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Command line parameters:

-MODEL-framet_p2n.model -DEV=xlp
-Q-cgn2_1/USPTO_spool/US10036041/runat_13012003_160808_7048/app_query.fasta_1.391
-DB=N_Geneseq_101002 -OFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=-LOCAL -OUTFMT=pto -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10036041_eCGN_1_1_79_@runat_13012003_160808_7048 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=10 -XGAPDEXT=0.5 -FGAPDP=6 -FGAPEXT=7
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*

//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*

//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*

//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*

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//SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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0 0 0 0 0 0 0	Gene encoding nove Human zacrp3 cDNA, Human cDNA encoding a no Human immune syste Gene encoding nove Skin cell cDNA, SE Rat cDNA isolated Mouse zacrp2 DNA, CDNA encoding rat cDNA encoding rat cDNA isolated Rat cDNA isolated Rat cDNA isolated Rat cDNA isolated Human protein havi Primer specific fo Human polynucleoti Human polynucleoti Human polynucleoti Human cDNA encodin	Description

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumours
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21-AUG-2000; 2000US-226517P.
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                                                                    ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu
                                                                                                                                                                LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly
                                                                                                                                                                                                                                                                                                                                                    MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys
GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln
                                              CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA
                                                                                                                                          AAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGC
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SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
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Xiang Z, Xie
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Claim 31; Page 107-109; 123pp; English.
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                                                                                                                                                                                                                            Human zacrp3; adipocyte complement related protein homologue; ACRP30; C1q domain; collagen-like domain; energy balance module cellular metabolism; metabolic disorder; obesity; anorexia; antimicrobial agent; infection; platelet aggregation inhibiti
                                                                                                                                                                                                                  adhesion; activation; vascular injury; antibacterial; antiviral;
                                                                                                                                                                                                                                                                                                                                  AAC64058 standard;
                   energy efficiency in mammals
                           Novel zacrp3 polypeptides used infections, for wound healing,
                                                                 WPI; 2000-665243/64.
                                                                                  Piddington CS,
                                                                                                                         20-APR-1999;
                                                                                                                                                                              WO200063377-A1
                                                                                                                                                                                                                                                                          Human zacrp3 cDNA,
                                                                                                                                                                                                                                                                                             19-FEB-2001
                                                                                                     (ZYMO ) ZYMOGENETICS INC.
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                                                        AAB29580
                                                                                                                                          2000WO-US10454
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                         99US-0294943
                                                                                  Bishop PD
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                           improving blood flow, and to analyze
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the human zacrp3 protein (AAB29580) and to CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue cc of adipocyte complement related protein (ACRP30) and contains a CC collagen-ilke domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a CC cterminal Clq domain comprising 10 beta-strands. The zacrp3 gene is CC located on chromosome 5p12. The invention also relates to zacrp3 gene is CC located on chromosome containing zacrp3 polypeptides, calls cc zacrp3-specific antibodies, expression constructs and host cells CC comprising zacrp3 nucleic acids, and methods of recombinant production of CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the CC anorexia, and conditions associated with these disorders such as obesity and CC anorexia, and conditions associated with these disorders may be useful CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful CC as antimicrobial agents, promoting lysis or phagocytosis of infectious CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion CC contains, antibodies and activity modulators may also be used to inhibit collagen. Induced platelet aggregation, adhesion, or activation, and may therefore be treat injury to the vasculature of the relation contains.
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HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe 120
                                                                                                                                                                                                                                                  GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGGCCCCCAGTATCA
                                                                            GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
                                                                                                                             ATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
                                                                                                                                            MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal
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CC which encode human secretory or membrane proteins represented by

CR AAB88317 - AAB8419. Included in the invention are primers

CA AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the

CC CDNA sequences of the invention. The invention also includes methods for

CC the production of antibodies directed against the proteins, and cDNA

CR sequences, which can be used in vaccines. The polynucleotide sequences

CC can be used in gene therapy. The polynucleotide sequences and the

CC proteins they encode may be used in the prevention, treatment and

CC diagnosis of diseases associated with inappropriate secretory

CC protein, membrane protein expression. The nucleic acids and complementary

CC sequences may also be used as DNA probes in diagnostic assays

CC (e.g. polymerrase chain reactions (PCR)) to detect and quantitate the

CC presence of similar nucleic acid sequences in samples. They may also be

CC used to study the expression and function of secretory proteins/membrane

CC polymeptides and their role in metabolism. The polymeptides may be used

CC as antigens in the production of antibodies against them and in assays to

CC identify modulators (agonists and antagonists) of expression and

CC agents to down regulate expression and activity. The antibodies may also
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                 acids encoding secretory proteins/membrane proteins, useful erapy or as candidate target molecules in drug development -
                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai T, Nishikawa
                                                                                                                                                                                                                                                                                                        SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
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23 - MAR - 1999;
24 - MAR - 1999;
31 - MAR - 1999;
05 - APR - 1999;
27 - APR - 1999;
04 - MAY - 1999;
04 - MAY - 1999;
04 - MAY - 1999;
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20-JUL-1999;
03-AUG-1999;
            The present sequence encodes a secreted or transmembrane polypeptide. The specification describes polypeptides designated PRO1484, PRO1334, PRO1122, PRO1889, PRO18890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990, PRO60300, PRO4424, PRO44080, PRO4408, PRO5737, PRO4425, PRO5990, PRO60300, PRO4424, PRO44022, PRO4400 and PRO44499, PRO1889 polypeptide is useful for diagnosing tumour in a mammal. The polypeptides, their agonists and antagonists are useful treating a condition associated with expression or activity of the polypeptide. Conditions treated include obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are capable of inducing proliferation of mammalian kidney mesangial cells and are therefore useful for treating kidney disorders associated with decreased mesangial cell function such as Bergers disease or other contracts of the polypeptides are capable of the polypeptides are capable of inducing proliferation of mammalian kidney mesangial cells and are therefore useful function such as Bergers disease or other capable of the polypeptides are capable of the polypeptides are capable of inducing proliferation of mammalian kidney mesangial cells and are therefore useful function such as Bergers disease or other capable of the polypeptides are capable of the polypeptides are capable of inducing proliferation of mammalian kidney mesangial cells and are therefore useful function such as Bergers disease or other capable of the polypeptides are capable of inducing proliferation of mammalian kidney disorders associated with correct properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
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Stewart TA,
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DB; AAB18909.
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                                                                                                                                                                                                                                                                                                                                                                                                          Fig 1; 222pp;
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Watanabe CK,
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77. 142
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Wood WI,
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Zhang Z;
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Best Local Similarity:
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          AAA95787 standard;
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                                                                                                               ArgMetGlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPhe
                                                                                                                                                                                                          TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys
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                                                                              LeuLeuPheGluThrLys
                                                                                                                                                 TCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGGATGAGGTTTGGCTG
                                                                                                                                                                                             TACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAA
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Alignment Pred. No.:

Sequence 1760

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Score:

Query

Percent Similarity: Best Local Similarity:

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Length:
Matches:
Conservative:
Mismatches:
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CC (IMOL) isolated as clone 1890540 from the Incyte BLADTOTO 11brary.

CC (IMOL) isolated as clone 1890540 from the Incyte BLADTOTOTO 11brary.

CC The human IMOLS (AAB15536-B1550) and their encoding polynucleotides

CC (AAA95775-A95789), and compositions comprising them are useful for the

CC diagnosis, treatment or prevention of immunological disorders.

CC infections and cell proliferative disorders associated with decreased

CC expression or activity of IMOL, such as immunological disorders

CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),

CC haematopoletic cancer, infections caused by virus (e.g. adenovirus,

CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,

CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.

CC plasmodium, Trypanosoma, intestinal protozoa), cell proliferative

CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and

CC cancers (e.g. actinic keratosis, arteriosclerosis, bursitis), and

CC cancers (e.g. beward, melanoma, sarcoma). The peptides are also

CC specifically recognizes these peptides. The polynucleotides may be used

CC specifically recognizes these peptides. The polynucleotides may be used

CC expression of IMOL may be correlated with the disease, as targets in a

CC compounds in drug screening techniques, Antibodies which specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianaemic; antiarteriosclerotic; antiasthmatic; antiabetic; nephrotropic; cance; antigout; dermatological; antihyroid; runcide; hepatotropic; antibod; immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial; gene therapy; diagnostic; immunological disorder; viral infection; ss; bacterial infection; fungal infection; parasitic infection; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
                                   compounds in drug screening techniques. Antibodies which specifically bind to IMOL may be used for the diagnosis of disorders characterized by expression of IMOL, or in assays to monitor patients being treated with IMOL or agonists, antagonists, or inhibitors of IMOL.
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                                     Human; secreted protein; membrane-associated protein; hypertension; inflammatory disorder; neurological disorder; haematopoietic disord skeletal developmental disorder; growth abnormality; autoimmune disorder; neurodegenerative disorder; nervous system disorder; bacterial infeperipheral myelinopathy; viral infection; cancer; obesity; diabetes hypotension; sexual development disorder; blood disorder; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human secre or membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and ameliorating various diseases such as inflammatory disorders (e.g. asthma), neurological disorders (e.g. dementia), haematopoietic disorders, skeletal developmental disorders, growth abnormalities, neurologenerative disorders (e.g. Huntington's disease), nervous sy disorders, autoimmune disorders (e.g. rheumatoid arthritis), peripheral myelinopathies, viral and bacterial infections, although the peripheral myelinopathies, viral and bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and hypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. ABK35582-ABK3569 represent the genes encoding the novel human secreted or membrane-associated proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumours
                                                                                                                                                                                                                                                                                                                                          Sequence 960
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                 Sleeman
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                 Murison
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cancer and neurological diseases and encoding polynucleotide used in the identification polypeptides used for treating inflammatory of genetic

Claim 1; Page 317-318; 352pp; English.

The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.

Sequence 1035 BP; 255 A; 242 Ç 298 <u>ლ</u> 240 Η, 0

Length: Matches:

US-10-036-041-2 (1-246) x AAC99776 Percent Similarity: Best Local Similarity: Match: 181 141 452 121 392 101 332 272 212 152 81 61 41 92 21 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGGCCCCCGTATCA ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT 3.06e-95 1311.00 97.15% 95.93% 95.90% (1-1035)Conservative: Mismatches: Gaps: Indels: 1035 236 3 7 0 631 180 160 140 100 451 120 331 80 40 151 200 511 391 60 211 271 20

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                                                                                                                                                                                                                      defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for
                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of cDN isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                   ACRP30; Clq domain; collagen-like domain; energy balance modulat cellular metabolism; metabolic disorder; obesity; anorexia; antinicrobial agent; infection; platelet aggregation inhibition; adhesion; activation; vascular injury; antibacterial; antiviral;
                                                        Mouse zacrp2; adipocy
ACRP30; Clq domain; c
cellular metabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising zacrp3 nucleic acids, and methods of recombinant production of carery3. Human zacrp3, and its agonists and antagonists may be used in the study and modulation of cellular metabolism and energy balance in mammals, and may therefore be used to treat disorders such as obesity and anorexia, and conditions associated with these disorders. Due to its Clq like domain, zacrp3 and zacrp3-containing fusion proteins may be useful as antinicrobial agents, promoting lysis or phagocytosis of infectious organisms such as bacteria or viruses. Zacrp3, its fragments, fusion proteins, antibodies and activity modulators may also be used to inhibit collagen-induced platelet aggregation, adhesion, or activation, and may therefore have potential for promoting blood flow within the vasculature of a mammal e.g., to treat injury to the vasculature or other collagenous clissue. Human zacrp3 and its antibodies may additionally be used to study dimerisation and oligomerisation. The present sequence represents DNA cereation and oligomerisation. The present sequence represents DNA cereation and oligomerisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue of adipocyte complement related protein (ACR930) and contains a collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and C-terminal Clq domain comprising 10 beta-strands. The zacrp3 gene is located on chromosome 5p12. The invention also relates to zacrp3 fragments, fusion proteins containing zacrp3 polypeptides, zacrp3-specific antibodies, expression constructs and host cells comprising zacrp3 models as a containing zacrp3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel zacrp3 polypeptides used to treat or prevent bacterial or viral infections, for wound healing, improving blood flow, and to analyze energy efficiency in mammals - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 115-117; 123pp; English.
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                                                                                                                                           MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys
                                                                                       LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly
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CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGGAACAATGGAGCTACTGGCCATGAA
                   ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu
                                                                     AAGTGTTGCCATGGAGATTATGGATTTCGTGGTTACCAAGGGCCCCCTGGACCTCCAGGT
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                                                                                                                                                                                                                                  29-APR-1998;
09-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HTV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AZS61606-Z61832 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences derived AAZ6166-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences AAZ61650-Z61688, AAZ6176-Z61812-Z61817-Z61829 encode proteins with one or more putative
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                                                                                                                                         GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
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                TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys
                                                                              GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal
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SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu

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Alignment Scores Pred. No.:
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                                                                                                                          dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences Az561006-z61802 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences Az56106-z61649, Az561725-z61765, Az561802-z61811 and Az561826 encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                  proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61812-Z61817 and AAZ61827-Z61829 encode proteins with one or more putative
                                         Sequence
                                                                                                                                                                                                                                                                                                          The invention relates
                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 137; 235pp; English.
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Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; keratinocyte growth stimulation; cancer; angiogenesis in
                                   Skin
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The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammantory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.
                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases \cdot
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DB; AAB55908.
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S-10-036-041-2 (1-246) x AAC99566 (1-1123)

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Length:
Matches:
Conservative:
Mismatches:
Indels:

140	WetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal		0 (
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120	101 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe	Qy 1	Ø
479	420 GGGCCAAGGGTGAGAAAGGAGACAAAGGCGACCTGGGGGCCTCGAGGGGAACGGGGCAG	Db 4:	D
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419	360 CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA	Db 31	D
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359	300 AAGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT	Db 31	D
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299	240 CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCCAGACTGCAGC	Db 2	U
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                                                                          The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of
                                                                                                                                                                                                                                                                                New isolated polynucleotide used in the identification disorders and encoding polypeptides used for treating disease, cancer and neurological diseases -
tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in
                                                                                                                                                                                                                                Claim 1; Page 176-177; 352pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound the protein and in modulating immune responses. The present sequence is a beautiful of the present sequence is a province of the province of the present sequence is a province of the present sequence of the present sequence of the present sequence is a province of the present sequence of the pre
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                                                                                                polynucleotides and polypeptides encoded by the polynucleotides lated from skin cells, useful for treating skin wounds, cancers, with and developmental defects, inflammatory diseases, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuPheGluThrLys 246
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Claim 1; Page 155-156; 466pp;

English

modulating immune responses

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention.
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Search completed: January 15, Job time : 304 secs 2003, 19:51:11

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MODEL=frame+_p2n.model -DEV=xlp
-Q-/Cgn2_1/USPTO_Spool/US10036041/runat_13012003_160809_7088/app_query.fasta_1.391
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST-45 -DDCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER-US10036041 @CGN_1_1_31 @runat_13012003_160809_7088 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys

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GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
ITILE OF INVENTION: Compositions Isolated From S
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FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
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APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Steman, Matthew APPLICANT: Onrust, Rene APPLICANT: Murison, James Gre TITLE OF INVENTION: Compositi
                                                                                      Sequence 217, Application US/09188930A Patent No. 6150502
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, James Greg
: Compositions
: and Methods F
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95.93%
95.90%
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Matches:
Conservative:
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; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 217
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-217
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Best Local Similarity:
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                                                                  LysHisGluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPhe 190
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                                                                                                                                                                                                                                                                                                                                          GlyProArgGlyGluArg------
CGCATTCGGACTTTTGACGCCAACACCGGCAACCACGACGTGGCCTCGGGCTCCACCATC
                     SerMetTyrSerTyrGluMetLys---GlyLysSerAspThrSerSerAsnHisAlaVal 209
                                                                                                                                                            CCCATCAAGTTTGACAAGATTCTGATGAATGAGGGAGGCCACTACAATGCATCCAGTGGC
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                                                    -CTGGCCATCGGCCTAGTGCACAATGGCCAG----TAC
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Conservative:
Mismatches;
Indels:
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61	Qy 42 CysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProdlyPro	
100	DD 100 GATGACGTTACTACAACTGAAGAGCTAGCTCCTGCTTTGGTCCCTCCC	
	24 AspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSe	
23 99	Qy 4 ArgGlnLeu1leTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuCysGln	
	US-10-036-041-2 (1-246) x US-08-463-911-1 (1-1276)	
	Alignment Scores: 5.98e-20 Length: 1276 Pred. No.: 299.00 Matches: 82 Score: 299.00 Matches: 82 Percent Similarity: 47.10% Conservative: 40 Best Local Similarity: 31.66% Mismatches: 103 Query Match: 21.87% Indels: 34 DB: 6aps: 9	
	EY: CDS ON: 46786	_
	HARACTERIS 1276 base nucleic aci	
	TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 1:	
	DOCKET ATION 1	
	nan, Patricia NUMBER: 32,227	
	CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:	
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	OPERATING SYSTEM: PC-UOS/MS-UOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 · CHERRUT APPLICATION DATA:	
	TYPE: Floppy disk R: IBM PC compatible	
	2173 READABI	
	STATE: Masachusetts COUNTRY: USA	
	; ADDRESSEE: Hamilton, Brook, Smith & Reymolds, F.C. ; STREET: Two Militia Drive · OTHY: Lexington	
	SEQUENCES: 7	
	INVENTION:	
	APPLICANT: Scherer, Philipp APPLICANT: Lodish, Harvey F	
	pplication 69330 RMATION:	
	Db 948 CTCTTCTACGACCCTTATTGGACCGACAGCCTGTTCACCGGCTTCCTCATCTAC 1001	м
	Qy 226 AlaLeuHisGlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243	2
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CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI9
TELECOMMUNICATION INFORMATION:
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                      CITY: Lexington
                                                                                                                                                                                                              ZIP: 0217:
                                                                                                                                                                                                                       COUNTRY:
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                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                        Massachusetts
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                                                                                                                                                                                                                          USA
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Lodish, Harvey F.
VENTION: A NOVEL SERUM PROTEIN PRODUCED
                                                                                                                                Patentin Release #1.0,
                                                                                                                                                                                                                                                                                  Hamilton, Brook,
                                                                                                                                                                                                                                                                                                                                 EXCLUSIVELY IN
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                 WHI95-05
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TrpLeuArgMet---GlyAsnGly-----AlaLeuHisGlyAspHisGlnArgPhe
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; NAME/KEY:
; LOCATION:
US-08-463-911-6
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base ~ Type.
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STRANDEDNESS: single
TOPOLOGY: linear
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AATAATGTGGACCAGGCCTCCGGCTCTGTGCTCCTGCATCTGGAGGTGGGCGACCAAGTC
                                                GlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluVal
                                                                                                             AAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACCTATGATCAGTACCAGGAA
                                                                                                                                                                    TyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLys
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
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SEQ ID NO 9
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
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ORGANISM: Homo
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GGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCTAT
                                                                                 SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThr
                                                                                                                            GCCTATGTATACCGCTCAGCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCAAC
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR US
FILE REFERENCE: 210121.475C1
CURRENT FILLING DATE: 1999-08-09
CURRENT FILLING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
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TYPE: DNA
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                                                            GGAGACTCCCGTAGCATGACCCCTGTGGATGTCCAGTGACAAATCCAGCAGCCACCATA
                                                                                                ArgGlyGluArgGlyGln---
                                                                                                                                        CAGGTGAGCAGCCCAGAA - - - AGAGACAACGAAACCTTTAACAGTGGTGACTCTGGACAA 228
                                                                                                                                                                              GlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyPro 94
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-LysGlyTyrProGlyIleProProGluLeuGlnIleAlaPheMetAlaSer 123
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GENERAL INFORMATION:
APPLICANT: Fischer et al.
APPLICANT: TUVENTION: 123 Human Secreted Proteins
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GENERAL INFORMATION:
APPLICANT: Sheppard, Paul
APPLICANT: Humes, Jacqueli
                                                 Sequence 1, Application Patent No. 6197930
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                                                                                                                                                                                                                                            uArgMet-----GlyAsnGlyAlaLeuHisGlyAspHisGlnArgPheSerTh 236
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS FILE REFERENCE: 97-49
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 PheAlaGlyPheLeuLeuPhe 243
                                   PhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrValTyr-----
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                                                                                                    AAGCCAGCCTCGCTCTCGGGGGGGGGCCATGGTGAGGCCTGGAGGACCAAGTGTGG
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                                                                  LeuArgMetGlyAsnGly---
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876

TTCTCCGGATTTCTGGTGTAC 896

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GENERAL INFORMATION:
APPLICANT: Leaby, K.
APPLICANT: Leaby, K.
APPLICANT: BOSSONE, S.
TITILE OF INVENTION: SECRETED PROTEINS AND US
TITILE OF INVENTION: SECRETED PROTEINS AND US
TITILE OF INVENTION: MUMBER: US/09/336,536
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                              LysGlyTyrProGly------IleProProGluLeuGlnIleAlaPheMetAlaSer 123
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   CTTGTCAAAAACGGGCAGTCCATCGCCTCTTTCTTCCAGTAT - - - TTTGGGGGGGTGGCCC
                                  LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGly-----
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                                                                                                                                        GAGCAGGGCCATTACGACCCCACTACTGGCAAGTTCACCTGCCAAGTGCCTGGCGTCTAC
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                                                                                                                                                                                                            GAGAGCCGGGTACCTCCGCCAGCCGACACCCCCTACCTTTCGACCGTGTGCTGCTAAAT
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US-09-336-536-8
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: Leiby, K
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Patent No. 6406884
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APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND
FILE REFERENCE: 7853-144
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TYPE: DNA
ORGANISM: Mus musculus
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                                    AsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGlyAspLys
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                                                                                                                           GAGAGCCGGGTACCTCCGCCAGCCGACACCCCCTACCTTTCGACCGTGTGCTGCTAAAT
                                                                                                                                                                                      Leu \verb|AlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIndex | See Foundation | S
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                                                                                                                                                                                                                                                                                                                     LysGlyTyrProGly-----IleProProGluLeuGlnIleAlaPheMetAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTGATGGCCGCGACGGTGCACCCGGGAGCTCCGGGAGAGAAAGGCGAGGGCGGGAGACCG
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18.80%
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Conservative:
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GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
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US-09-188-930-30
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Best Local Similarity:
Query Match:
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SEQ ID NO 30
LENGTH: 1015
TYPE: DNA
ORGANISM: Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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813 TTCTCTGGATTTCTCGTCTAT 833
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                                                                                                                                                                                                                                      251 ---TCAGGCTCTCCTCCTGGACGACAACAAGATCCCCAGCCTGTGTCCCCGGGCAG--- 304
                                                                                                   359 GACGGCCGTGATGGCCGCGACGGTGCACCCGGAGCTCCGGGAGAGAAAGGCGAGGGCGGG 418
                                                      68 HisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGly 87
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                                                                                                                                                                                                    GlnThrGlyGlyLeuProProAspCysSerLys------CysCysHisGlyAspTyr 47
                                                                                                                                   SerPheArgGlyTyrGlnGlyProProGlyProProGlyProProGlyIleProGlyAsn
AspLysGlyAspLeuGlyProArgGlyGlu-----ArgGlyGlnHisGlyProLys 104
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254.50
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Indels:
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yAspTyr 47	ysCysHisGl	rLysC	lyGlyLeuProProAspCysSerLy	GlnThrGlyGlyLe	31	Qy	
Pro 3	luTyrMetGluSer	sLeuCysGlnAspG A	LeuAlaLeuPhePheLeuProPheCysLeuCy TGCCCTGCTGCTTCTGGGTCTGGCA	LeuLeuAlaLeuP CTTCTTGCCCTGC	11 207	Оу	
		-218 (1-1001)	x US-09-188-930-	-041-2 (1-246)	10-036	us-	
	1001 79 35 100 35	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1.31e-15 252.50 45.78% 31.73% 38.47%	cores: ilarity: Similarity:	TC Pane	Align Pred. Score Perce Best Query DB:	
		3.0	s Versio	FILING DATE: FILING DATE: PEQ ID NOS: FastSEQ for 218 1001 NA NA Rat MM: Rat	CURRENT FII NUMBER OF S SOFTWARE: F SEQ ID NO 21 LENGTH: 10 TYPE: DNA ORGANISM: -09-188-930	US- S	
	n Cells	plated From Skin Their Use	eg ions Isc ods For	Murison, WVENTION: WVENTION: ENCE: 1100	APPLICATITLE OF TITLE OF TITLE OF THE REPORT OF THE PRESENTE O		
			s D. rna thew	Watson, strachan sleeman, Onrust, 1	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	٠.	
			ion US/09188930A	930-218 218, Applicat o. 6150502 INFORMATION:	ULT 13 09-188-9 lequence atent No	33. S3.	
		0 3	24 91	SerThrPheAlaGlyPheLeuLeuPhe ::: :::::: AGTACCTTCTCTGGATTTCTCGTCTAT	235 884	Qy Db	
rgPhe 234 CAGAC 883	lyAspHisGlnAr ::: CCAGCATCAAAAC	AlaLeuHisGlyAspHis :::::: ATTGGCATCTATGCCAGCATC	TrpLeuArgMetGlyAsnGlyAla ::::::: ATGGGTTCAGGTGGGTGTGGGTGATTACATTGGC	ValTrpLeuArgMetGlyAsnGly ::::::: GTATGGGTTCAGGTGGGTGTGGGT	218 824	Оy	
pGlu ::: CCAG	laLy AACC	AlavalLeuLysLeuAlaLys :::::::: CGATGGTGAGGCTAGAACCT	LysSerAspThrSerSerAsnHisAlaValLeuLysLeuA 	TGGCCAAAGCCAGCC	200 764	Qy Db	
•••	1 u	PheSerMetTyrSe ::: GCTTCTTTCTTCCA	LeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrG ::: :::::: TTTGATCTTGTCAAAAATGGCCAATCCATAGCTTCTTTCT	LeuMetHis ::: TTTGATCTTGTCAAA	182 707	Фу	
alTyr 181 :: TACAG 706	uGluValTyrValTyr ::: .CCGGGCCAGCCTACAG	HisgluaspvalGluGluValTyrValTyr 	SerMetMetLys	ValTyrPhePheThrPhe GTCTACTACTTTGCTGTC	162 659	Оy	
erGly 161 CTGGT 658	GlyAlaProValSerGly ACCTGCCAAGTGCCTGGT	ThrGlyArgPheGl ::: ACCGGCAAGTTCAC	hrasnIleGlyasnPhePheAspValMetThrGlyArgPhe 	ThrAsnIleGlyAsn CTCAATGAGCAGGGA	142 ' 599 '	Оу	
rGCTG 598	ePheSerSerVa	lnAsnSerGlyIleIlePheSerSerValGlu 	erAsnG	AlaSerLeuAlaThrHisPheS ::: CGATCANAGAGCCGGGTACCTC	122 i	Qy Db	
	OGIULEUGINILEALAFHEMEC 	ITEPTOPTOGIULEUGIDILEATAFHENEC -:- GTGCCCCCACGATCAGCCTTCAGTGCCAAG	GAGTGCT	GlyGluLySGlyTyrProGly GGGGCTATCGGGCCTGCGGGG	105.0	рь .	
TGTG 478	:::	CCGGGCCGCGTGGAG	CGTGGGGAG			Db	

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RESULT 14
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 Query Match:
               Best Local Similarity:
                             Percent Similarity:
                                              SCOLE:
                                                            Pred. No.:
                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 728
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09336536 Patent No. 6406884
                                                                                                                                                                                                                                    APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND
FILE REFERENCE: 7853-144
                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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251.00
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Mismatches: Indels:
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                                                                                         SEQ ID NO 1
LENGTH: 1338
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                                                                                                                              CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                             APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
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Best Local Similarity:
Query Match:
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                       PheAlaGlyPheLeuLeuPhe 243
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: January 15, 2003, 21:21:52 Job time: 77 secs

GenCore version 5.1.3 Coppright (c) 1993 - 2003 Compugen Ltd.

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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             GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
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WLRMGNGALHGDHQRFSTFAGFLLFETK"
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AF329837
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                                                                    Direct Submission
Submitted (200-DEC-2000) Bioinformatics,
Eastlake Ave. East, Seattle, WA 98102,
Location/Qualifiers
                                                                                                                 2 (bases 1 to 1710) Piddington, C.S. and Direct Submission
                                                                                                                                                               Homo
                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1710)
Piddington, C.S. and Bishop, P.
                                                                                                                                                                                                                                                                              1710 bp mRNA linear PRI 1: Homo sapiens complement-clq tumor necrosis factor-related (CTRP3) mRNA, complete cds.
                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                              sapiens complement-clq
                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
            /map="5p13-p12"
l. .1710
                                                                                                                                                                                                                                                          GI:13274519
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Primates;
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//db_xref="GI:13374520"
//db_xref="GI:13374520"
//transfation="MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCH/transfation="MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQCEPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERQOHGGXSFRGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGYFFTFSMMKHEDVEEVYVYLMHNGRTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEV
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Oncology, Graduate School of Dentistry,
Yamadaoka, Suita, Osaka 565-0871, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Maeda, T., Hayashi, A. and Saito, T.
Molecular cloning, chromosomal lo
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/db_xref="GI:14586743"
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77. .817
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/db_xref="taxon:9606"
/chromosome="5"
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Sequence 11 from
Ax039955
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Piddington, C.S. and Bishop, P.D.
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                                                                                                     /protein_id="CAC16633.1"
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/db_xref="GI:11229977"
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GVYFFTFSMMKHEDVEEVYYYLMHNGNTVFSMYSYETKGKSDTSSNHAVLKLAKGDEV
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272 c 293 g 268 t
                                                                                                                                                                                                              /organism="Mus musculus"
/db_xref="taxon:10090"
1111. .851
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Eutheria; Rodentia; Sciurognathi; Muridae;
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Mus musculus
Eukaryota; Metazoa; Chordata; C.
Manmalia; Eutheria; Rodentia; S.
1 (bases 1 to 1879)
Maeda,T., Abe,M., Kurisu,K., Ji
Molecular cloning and character
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                                                                                     Mus musculus collagenous repeat-containing protein (CORS26) mRNA, complete cds. AF246265
AF246265.1 GI:11275676
                                                                   musculus
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Sciurognathi; Muridae
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                                MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal
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                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding a putative secretory protein and in skeletal development J. Biol. Chem. 276 (5), 3628-3634 (2001) 21264842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-MAR-2000) Radiology and Radiation Oncology, University School of Dentistry, 1-8 Yamadaoka, Suita, Osa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maeda, T. and Jikko, A. Direct Submission
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PKGEKGYPGVPFELQ1AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVS
GVYFFTFSMKKHEDDKEEYYVLMHNGNFVFSMYSYETKGKSDTSSNHAVLKLAKGDEV
WLRMGNGALHGDHQRFSTFAGFLLFETK"

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Kato,S. and Kimura,T.
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PQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKG
DKGDLGPRGERGQHGPKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIG
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/db_xref="GI:15209728"
/translation="MLWRQLIYWQLLALFFLPFCLCQDEYMEVSGRTNKYVARIVQSH
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Mammalia; Eutheria; F
1 (bases 1 to 810)
Ota,T., Isogai,T., Ni
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Sequence
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AX136588.
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Secretory protein or membrane protein Patent: EP 1067182-A 510 10-JAN-2001;
               Hayashi,K.
                                                               human
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                       Nishikawa, T.,
                                      Chordata;
Primates;
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EP1067182.
                                      Craniata; Vertebrata; Catarrhini; Hominidae
                       Kawai,Y.,
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                       Sugiyama, T.
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SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu
                               TyrLeumetHisAsnGlyAsnThrValPheSermetTyrSerTyrGlumetLysGlyLys
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sapiens, Similar to complement-clq tumor necrosis or-related protein; likely ortholog of mouse CORS26 agenous repeat-containing sequence of 26-kba protein), clone 17511 IMAGE:4720611, mRNA, complete cds.
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s: IRAL Plate: 38 Row: p Column: 18.
    Location/Qualifiers
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ct: amadan@systemsbiology.org
Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e, Mark Ketteman and Anuradha Madan
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Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
equencing by: Institute for Systems Biology
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ct: MGC help desk
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                                                                                     /product="Similar to complement-clq tumor necrosis factor-related protein; likely ortholog of mouse CORS26 (collagenous repeat-containing sequence of 26-kDa
                                                                 protein)"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 546)

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Baker,K.P., Goddard,A. and Wood,W.I.

Human polypeptides and methods for the use thereof

Patent: WO 0107611-A 240 01-FEB-2001;
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GNGALHGDHQRFSTFAGFLLFETK"
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Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc.,
Eastlake Ave. East, Seattle, WA 98102, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1306) Piddington, C.S., She
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/db_xref="taxon:9606"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
                                                                                                                                                                                                                     Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                               Submitted (25-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC022187 3959 bp mRNA linear PRI 28-
Homo sapiens, complement-clq tumor necrosis factor-related
7, clone MGC:26871 IMAGE:4825040, mRNA, complete cds.
                                       contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin He
Madan, Stephanie Rodrigues, Amy Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Clone
                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC022187.1 GI:18381162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iomo sapiens
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  distribution:
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  MGC
  clone
                                         Erin Helton,
Amy Sanchez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
  distribution information
                                            and Michelle Whiting
                                                                   Mark Ketteman,
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  can
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 LeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGluSerProGlnThrGly
  GlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspVal
                                              TGTGGAAGCATCGTGCTCAAATCCGCCTTTTCTGTTGGCATCACAACCAGCTACCCAGAA
                                                                                                                                    CCTGGACCAAAGGGAGACAGAGGAGAACAAGGGGACCCGGGGCTGCCTGGAGTTTGCAGA
                                                                                                                                                                                                                            GGGAAGAAGGACCCATAGGACCAGAGGGAGAGAAAGGAGAAGTAGGTCCAATTGGTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through the I.M.A.G.E. Consortium/LLNL Series: IRAK Plate: 33 Row: k Column: 8
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PPGANGSPGPHGRIGLPGRDGRDGRKGEKGEKGTAGLRGKTGPLGLAGEKGDQGETGK/
KGPIGPEGEKGEVGP1GPPGPKGDRGEQGDPGLPGVCRCGSIVLKSAFSVGITTSYPE
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/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
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/db_xref="taxon:9606"
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/db_xref="GI:18381163"
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234. .1103
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Search completed: January 15, 2003, 20:42:58 Job time : 3099 $\sec s$

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Command line parameters:

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-MODEL-frame+_p2n.model -DEV-xlp
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-O_-Ggn2_1/USPTO_Spool_VIS10036041/runat_13012003_160809_7069/app_query.fasta_1.391
-OB=EST -OPMT=fastap -SUFFIX=P2n.rst MINMATCH=0. LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MN=0 -ALIGN=15 -NODE-LOCAL
-OUTFMT=200 -THR_SCORE-pct -THR_MAX=100 -THR_MN=0 -ALIGN=15 -NODE-LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-OS10036041_eCGN_11_1_1716_@runat_13012003_160809_7669 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LOWLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

AUTHORS TITLE	Sections	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BM924169	RESULT 1
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST.	BM924169.1 GI:19374548	BM924169	5', mRNA sequence.	AGENCOURT_6630525 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5760396	BM924169 1103 bp mrNA linear EST 12-MAR-2002		

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Tissue Procurement: Life Technologies,
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Contact: Robert Strausberg, Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone="IMAGE:5760396"
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/lab_host="DH10B"
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Tissue Procurement: Life Technologies,
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Plate: LLAM11500 row: o column: 23
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                            /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb, Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library.*
                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:5199982"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
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                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 1007)
                                                                                      BQ958105
BQ958105.1 GI:22373583
EST.
                                                                house mouse.
Mus musculus
                                                                                                                       AGENCOURT_10013971
IMAGE:6486507 5', r
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Unpublished
          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
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Sciurognathi; Muridae;
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Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA. Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC Clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa:
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
a 236 c 280 g 231 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
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/strain="FVB/N-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., F.
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., F.
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI956432 724 bp mRNA linear EST 20-AUG-
ul77b06.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2136563 5' similar to SW:CERL_RAT P98087 CEREBELLIN-LIKE
GLYCOPROTEIN. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                             MGI:1001239
                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free tl
TMAGE Consortium (info@image.linl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI956432.1
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quality sequence stop: 51
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                                                                   (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATCTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI show be used to isolate the cDNA insert Size selection was
 primer CGACCTGCAGCTCGAGCACA.
             Institute of Medical Science). Custom primers sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG
                                         constructed by Dr. Sumio Sugano (University of Tokyo
                                                     performed to exclude fragments <1.5kb.
                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                       /note="Organ: kidney; Vector: pME18S-FL3;
                                                                                                                                                                                   /lab_host="DH10B"
                                                                                                                                                                                                                  /sex="
                                                                                                                                                                                                                            /clone_lib="Sugano mouse
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/clone="IMAGE:2136563"
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US-10-036-041-2 (1-246) x AI956432
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                                                                                                                                                                                                                                                                                                       LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
                                                                                                                                                                                                                                                                                                                                                                                                TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys
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Wistow,G., Bernstein,S.L., Wyatt,M.K., RayJ.W., Bouffard,G., Smith,D. and Peterson Expressed sequence tag analysis of human
                                                                                                                                                                                         BQ637986
hd17a10.yl Human Retina
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                                                                    Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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                  Wyatt,M.K., Ray
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MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
                                                                                                                            GGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAG
                                                                                                                                                                                                       CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAA
                                                                                                                                                                                                                                                                                                                                                                          CTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCCCAGACTGCAGT
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                                          CATGGCCCCAAAGGAGAGAGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC
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6/331, NIH, Bethesda, MD
Tel: 301 402 3452
Fax: 301 496 0078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wistow G
Section on Molecular Structure and Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: graeme@helix.nih.gov
Plate: 17 row: a column: 10
Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pSPORT1 vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'. pgAcryAcTyCTyAcTYCTACATCGGACGCGCGCCC(T)]15-3'

]. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: Eye; Vector: pspoRT1; Neural retina tissue was dissected from two 80 year old donors with no observed eye disease. 100ug of total RNA was used for library construction. A directionally cloned cDNA library in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hd17a10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Retina"
/dev_stage="Adult"
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RESULT 6
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AI006567

MRNA linear EST 12-JUN-
uel4d08.yl Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1480335 5' similar to SW:CERL_RAT P98087 CEREBELLIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity Seg primer: primer name ambiguous High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 692)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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314 286 1810
                                       /note="vector: pME185-FL3; Site_1: DraIII (CACTGTGTG);
/note="vector: pME185-FL3; Site_1: DraIII (CACTGTGTG);
Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCCTACTGG], digested and cloned into distinct DraIII
sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTGCTCTTAAAAGCTGCG and 3' end primer
CGACTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1480335"
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                    Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                      A1527737
680 bp
uj28e09.yl Sugano mouse kidney i
IMAGE:1921288 5', mRNA sequence
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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University School
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1035.00
95.88%
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75.71%
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US-10-036-041-2 (1-246) x AI527737
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ATGGCTTCTCTAGCAACTCAC-
                          MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140
                                                        CATGGCCCCAAAGGAGAAAGGCTACCCCAGGGTGCCACCAGAACTGCAGATTGCATTC
                                                                    HisGlyProLysGlyGlúLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free IMAGE Consortium (info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Forest Park Parkway, Box 8501, 314 286 1800
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/sex="female"
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GluSerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyr 47
                                                                                                                      Scores:
                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631 bp 602114255F1 NCI_CGAP_Kid14 Mus r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                quality sequence stop: 623.
                                                                                                                                                /Strain="vb/N
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:4242612"
/clone=Lib="NCI_CGAP_Kid14"
/clone=Lib="NCI_CGAP_Kid14"
/lab_host="MIDB (T1 phage-resistant)"
/lab_host="MIDB (T1 phage-resistant)"
/note="organ: kidney; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | "
31 a 154 c 176 g 120 t
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/strain="FVB/N"
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Sciurognathi;
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                                                                                                                                                                                                                                                                     Mus musculus
Bukaryota; Metazoa; Chordata; Craniata;
Bukaryota; Butheria; Rodentia; Sciurogna
                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                       631 bp 602110304F1 NCI_CGAP_Kid14 Mus n 5', mRNA sequence.
BF784596
BF784596.1 GI:12089632
                Plate: LLAM9850 row: g column: High quality sequence stop: 629.
                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 631)
Location/Qualifiers
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Sciurognathi; Muridae;
                                                                                                                                                                                                                               Mammalian
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RESULT 10
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                                                                                                                         un02e01.yl Sugano mouse kidney mkia Mus IMAGE: 2372664 5' similar to SW:CERL_RAT GLYCOPROTEIN. ;, mRNA Sequence
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                       nouse mouse
musculus
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/clone_lib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
/note="Organ:
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Wilson, R. and Wilson, R. an
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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77 a 172 c 156 g 146 t 5 others
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/clone_lib="Sugano mouse
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Location/Qualifiers
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/lab_host="DH10B"
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Schurk, R.,
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                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagj,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                              Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
On Nov 30, 2000 this sequence version replaced gi:11468663.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Contacts of Contacts (2002)
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                       Computer-based methods for the mouse full-length cDNA
                                        Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Y. and Hayashizaki,Y.
                                                                                                                        RIKEN integrated sequence analysis (RISA) system -- 384 - format
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Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I
K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Project of Genome Exploration Research Group in Rik
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/tissue_type="head"
/dev_stage="0 day neonate"
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/clone="4833401011"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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BB649178 RIKEN full-length enriched, 16
musculus cDNA clone C130060D14 5', mRNA
BB649178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
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Muramatsu,M. and Hayashizaki,Y.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA
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                                                               GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/lab_host="DH10B"
/note="Site_1: SalI; Site_2:
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transcriptase and subsequently enriched for full-length
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/clone="C130060D14"
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/strain="C57BL/6J"
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/dev_stage="16 days
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watchiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and hayashizaki,Y.
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagamai, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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BB610546 RIKEN full length enriched, adult
cDNA clone 2310005P21 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                        encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fikuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                          Hayashizaki,Y.
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                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with luman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           and Hayashizaki, Y
                                                                                                                                                                               tissues.
                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
                                                               /clone="2310005P21"
/tissue_type="tongue'
                                          /clone_lib="RIKEN full-length
                                                                                                                                                     ocation/Qualifiers
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                                                                                                                            GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180
                                                                                                                                                                           GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGGGAGATTTGGGGGCCCCCTA-TCA
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mkia

musculus cDNA clone

EST 17-DEC-1998

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JOURNAL COMMENT
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                                        MetLeuTrpArgGlnLeuIleTyrTrpGlnLeuLeuAlaLeuPhePheLeuProPheCys
                                                                                                                         ATGCTCGGGAGCACCTGGTGGCACCTGCCTTTGCTTTCCTCCATTTTGC
LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly 60
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AI316916
AI316916.1 GI:4032183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 571)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: kidney: Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 GlyAlaLysGlyGluLysGlyAspLysGlyAspLeuGlyProArgGlyGluArgGlyGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 828)
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                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1331 row: h column: 14
High quality sequence stop: 740.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:4592701"
/clone="IMAGE:4592701"
/clone=lib="NIH_MGC_75"
/clone=lib="NIH_MGC_75"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); 5' and
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGCCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTACAGGCCGACACGCCGACATG-dT[30]BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4, 0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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s cDNA clone IMAGE:4592701
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Percent Similarity:
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CA). Note: this is a NIH_MGC Library."
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Matches:
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Search completed: January 15, 2003, 21:20:27 Job time: 2243 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgp2_1/USPTQ_Spool/US10036041/runat_13012003_160809_7112/app_query.fasta_1.391
-Q-/cgp2_1/USPTQ_Spool/US10036041/runat_13012003_160809_7112/app_query.fasta_1.391
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -ENND-1 - MATRIX-blosum62
-TRANS-Pumman40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US10036041_eCGN _11_36_erunat_13012003_160809_7112
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOF=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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quence 46, Appl quence 61, Appl quence 61, Appl quence 46, Appl quence 46, Appl equence 51, Appl equence 51, Appl equence 151, Appl equence 151, Appl	Sequence 85, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

ALIGNMENTS

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US-10-036-041-1
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                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P93030R1C8 CURRENT APPLICATION NUMBER: US/10/036,041 CURRENT FILING DATE: 2001-12-26
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APPLICANT: 'Eaton, Dan L.
APPLICANT: Goddard, Audr
                 PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
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APPLICATION NUMBER: 60/113430
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LENGTH: 17
TYPE: DNA
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FILING DATE: 2000-03-02
APPLICATION NUMBER: PCT/US00/14042
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              GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer
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                                           HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuglnIleAlaPhe
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APPLICATION NUMBER: FILING DATE: 2001-0

2001-06-29

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DR FILING DATE: 2000-12-20
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DR FILING DATE: 2001-03-22
DR APPLICATION NUMBER: 09/854208
DR FILING DATE: 2001-05-10
DR APPLICATION NUMBER: 09/854280
DR APPLICATION NUMBER: 09/854280
DR FILING DATE: 2001-05-10

APPLICATION NUMBER: 09/747259 FILING DATE: 2000-12-20 APPLICATION NUMBER: 09/644848 FILING DATE: 2000-08-22

FILING DATE:

1999-08-25

APPLICATION NUMBER: 09/380142

FILING DATE:

APPLICATION NUMBER: 09/311832 APPLICATION NUMBER: 60/162506

1999-05-14

LING DATE:

1999-10-29

APPLICATION NUMBER: 60/138166 FILING DATE: 1999-06-08 APPLICATION NUMBER: 60/144791 FILING DATE: 1999-07-20

APPLICATION NUMBER: 60/146970 FILING DATE: 1999-08-03

FILING DATE: 1999-05-04
APPLICATION NUMBER: 60/135750

LING DATE:

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APPLICATION NUMBER:

60/132383

APPLICATION NUMBER: 60/132379 FILING DATE: 1999-05-04 FILING DATE: 1999-04-27 APPLICATION NUMBER: 60/132371 FILING DATE: 1999-05-04

APPLICATION NUMBER: 60/131272 FILING DATE: 1999-04-27 APPLICATION NUMBER: 60/131291 APPLICATION NUMBER: 60/131270 FILING DATE: 1999-04-27 APPLICATION NUMBER: 60/130359 FILING DATE: 1999-04-21

FILING DATE:

FILING DATE:

1999-03-31

APPLICATION NUMBER: 60/127035

1999-03-24

APPLICATION NUMBER: 60/125826

1999-03-23

60/125778

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FILING DATE: 1999-0: APPLICATION NUMBER:

APPLICATION NUMBER: 60/125774

1999-03-23

FILING DATE:

APPLICATION NUMBER: 60/116843 FILING DATE: 1999-01-12 APPLICATION NUMBER: 60/115552 APPLICATION NUMBER: 60/114140 APPLICATION NUMBER: 60/113621

1999-01-

APPLICATION NUMBER: 60/129122 APPLICATION NUMBER: 60/127706 FILING DATE: 1999-04-05

1999-04-1

APPLICATION NUMBER: 09/874503 FILING DATE: 2001-06-05

DR APPLICATION NUMBER: 09/908,827
DR FILING DATE: 2001-07-18
DR APPLICATION NUMBER: PCT/US99/10733
DR FILING DATE: 1999-05-14
DR APPLICATION NUMBER: PCT/US99/28551
DR FILING DATE: 1999-12-02
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PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
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PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/11440
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/11552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/11552
PRIOR APPLICATION NUMBER: 60/116843
PRIOR APPLICATION NUMBER: 60/115774
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR PILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125778
PRIOR APPLICATION NUMBER: 60/125778
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030RIC4
FILE REFERENCE: P3030RIC4
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CURRENT FILING DATE: 2001-12-26
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                                                                                                   FILING DATE: 1999-03-24
APPLICATION NUMBER: 60/
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Godowski, Paul J.
Gurney, Austin L.
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APPLICATION NUMBER: 60/135750
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                                               FILING DATE: 2001-06-01
APPLICATION NUMBER: PCT/US01/19692
FILING DATE: 2001-06-20
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APPLICATION NUMBER: PCT/US00/34956
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FILING DATE: 2001-02-28
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APPLICATION NUMBER: PCT/US99/28551
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PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR PELICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
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PRIOR PELICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR PELICATION NUMBER: 60/113621
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PRIOR APPLICATION NUMBER: 60/125774
PRIOR APPLICATION NUMBER: 60/125778
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125826
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/127035
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APPLICANT: Eatcon, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin
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PRIOR APPLICATION NUMBER: 60/131272
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CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
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R FILING DATE: 1999-08-03
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TYPE: DNA
ORGANISM: HOMO
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APPLICATION NUMBER: 09/854208
FILING DATE: 2001-05-10
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APPLICATION NUMBER: 09/747259
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LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40
                                               Sapien
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Matches:
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                                  SOFTWARE: PatentIn Ver. SEQ ID NO 359
                                                                                                                                              APPLICANT:
                                                                                                 APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
09-822-849A-359
                                                   PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
                                                                               CURRENT APPLICATION NUMBER: US/09/822,849A CURRENT FILING DATE: 2001-09-04
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        ORGANISM: Homo sapiens
                  TYPE: DNA
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                                                                                                                                                                                    Clark,
                                                                                                                                     Howes, Steven H.
Resnick, Richard J.
Gulukota, Kamalakar
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APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20020111302Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 799
CURRENT APPLICATION NUMBER: US/09/728,952
CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SOFTWARE: pt_fL_genes Version 2.0
SEQ ID NO 85
LENGTH: 1297
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (80)...(949)
US-09-728-952-85
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Query Match:
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Wang, Jian-Rui
Wang, Dunrui
Yamazaki, Vicki
Ujwal, Manusha L.
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Best Local Similarity:
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PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/776,976 CURRENT FILING DATE: 2001-02-05
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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                      SerAsnGlnAsnSerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePhe 148
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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
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PRIOR FILING DATE: 2000-04-13
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PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
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US-10-036-041-2 (1-246) x US-09-909-547-3 (1-1276)
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APPLICANT: Ericks
APPLICANT: Yen, I
APPLICANT: Bihair
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PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
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CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/776,976
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             CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR PELICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR PELICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09776976
Patent No. US20020037849A1
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and
                                                                                                                                                                                                     FILE REFERENCE: 76.US4.REG
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; LENGTH: 4517
; TYPE: DNA
; ORGANISM: HOMO :
US-09-776-976-5
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SOFTWARE: Patent.pm
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                                                                              GlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
                                                                                                                                                AlaLysGlyAspGluValTrpLeuArgMet---GlyAsnGly------AlaLeuHis 228
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                                                                                                                               GAGGTGGGCGACCAAGTCTGGCTCCAGGTGTATGGGGGAAGGAGCGTAATGGACTCTAT
                                                                                                                                                                                                                            TyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHisAlaValLeuLysLeu 212
                                                                                                                                                                                                                                                                                         GluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMet 192
                                                                                                                                                                                                                                                                                                                                                           GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMetLysHis 172
                                                                                                                                                                                                                                                                                                                                                                                            ATGCCCATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTATGTATACCGCTCAGCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCCAAC 407
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fruebis, Joachim APPLICANT: Erickson, Mary F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patent.pm
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ORGANISM: Homo
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CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 ProLysGlyGluLysGlyTyrProGlyIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 GGCCATAATGGGGCCCCCAGGCCGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 GlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLysGlyGluLysGlyAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysGlyAsp------LeuGlyProArg------GlyGluArgGlyGlnHisGly 102
                                                                                                                                            GlyArgPheGlyAlaProValSerGlyValTyrPhePheThrPheSerMetMetLysHis 172
                                                                                                                                                                                                                            ATGCCCATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACCACTATGATGGCTCCACT
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                                                  GluAspValGluGluValTyrValTyrLeuMetHisAsnGlyAsnThrValPheSerMet 192
                                                                                                              GGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACACATCACAGTCTAT
                                                                                                                                                                                                                                                                                  SerGlyIleIlePheSerSerValGluThrAsnIleGlyAsnPhePheAspValMetThr 152
                                                                                                                                                                                                                                                                                                                                          GCCTATGTATACCGCTCAGCATTCAGTGTGGGGATTGGAGACTTACGTTACTATCCCCAAC
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    ATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGGCTATGCTCTTCACC

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APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
APPLICANT: Bihain, Bernard
APPLICANT: Bihain, Bernard
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PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                           GlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGluGlyAlaLySGlyGluLySGlyAsp 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyAspHisGlnArgPheSerThrPheAlaGlyPheLeuLeuPhe 243
AAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGTGAAACCGGAGTACCCGGG
                                   LysGlyAsp---
                                                                      GGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACCCCTGGTGAGAAGGGTGAG
                                                                                                                                                                                                                           AAACCACGACTCAAGGGC---
                                                                                                                                                                                                                                                          SerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSer 48
                                                                                                                                                                                                                                                                                                     TGGGAGCTG----
                                                                                                                                                                                                                                                                                                                                    TrpGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGlu
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                                   -LeuGlyProArg-----GlyGluArgGlyGlnHisGly
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                                                                                                                                              CCTGCACAGGTTGGATG-GCGGGCATCCCAGGGCATCCG
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                                                                            US-10-036-041-2 (1-246) x US-09-964-824A-235 (1-4517)
                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: Patentin version 3.0
SEQ ID NO 235
LENGTH: 4517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 235, Application US/09964824A Patent No. US20020102531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/964,824A CURRENT FILING DATE: 2001-09-27 PRIOR APPLICATION NUMBER: US/60/236,033 PRIOR EILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: US/60/236,032 PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Horrigan, Stephe
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 689290-73
                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                  TrpGlnLeuLeuAlaLeuPhePheLeuProPheCysLeuCysGlnAspGluTyrMetGlu
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SerProGlnThrGlyGlyLeuProProAspCysSerLysCysCysHisGlyAspTyrSer 48

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APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Us
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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US-09-776-976-1
            NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09776976
Patent No. US20020037849A1
GENERAL INFORMATION:
APPLICANT: Fruebis, Joachim
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Fruebis,
APPLICANT: Erickso
APPLICANT: Yen, Fr
                                                                                 Sequence 1, Application US/09758055 Patent No. US20020058617A1
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Erickson, Mary Ruth Yen, Frances

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SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 1152
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PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR EILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR ETLING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
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                               ThrValPheSerMetTyrSerTyrGluMetLysGlyLysSerAspThrSerSerAsnHis
                                                                                                                                       TATGACAACAGCACTGGCAAGTTCTACTGCAACATTCCGGGACTCTACTACTTCTCTTAC
                                                                                                                                                                                                         GAGCCTGGAGAAGCCGCTTATGTGTATCGCTCAGGCCTTCAGTGTGGGGGCTGGAGACCCGC
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                                                                 CACATCACGGTGTAC----ATGAAAGATGTGAAGGTGAGCCTCTTCAAGAAGGACAAG
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PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/758,055 PRIOR FILING DATE: 2001-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/776,976 PRIOR FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/909,547 CURRENT FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and
FILE REFERENCE: 76.056.CIP
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TYPE: DNA
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272 GTTGGAATGACAGGAGCTGAAGGGCCTCGGGGCTTCCCCGGAACCCCTGGCAGGAAAGGA 331
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                                 ---GlyGlnHisGlyProLysGlyGluLysGlyTyrProGlyIleProProGlu-----
                                                                         GGAGAGAAGGGAGAGAAAGGAGATTCAGGTCTTCTTGGTCCTAAGGGTGAGACAGGAGAT
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Search completed: January 15, 2003, 21:23:46 Job time : 106 secs

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAI61016	ABK35221	AAD12584	AAI59230	AAI99523	AAF93874	AAC64058	AAA95787	AAA96336	ID
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	. Novel human protei	Novel human protei	Novel human protei	Human genset metab	Human polynucleoti	Human colon tumour	Human zacrp7 degen	Human secreted pro	Human genome-deriv	Probe #21834 used	3	Human brain expres	Human foetal liver	Human genome-deriv	Probe #8755 used t		Human brain expres	Human foetal liver			Human secreted pro	Human secreted pro	Primer specific fo	Human zacrp3 degen	Gene encoding nove	Mouse zacrp2 DNA,	Rat cDNA isolated	۳.	cell cDNA,	Skin cell cDNA, SE	ra	cDNA encoding rat		cell cDNA	encoding no	Primer specific fo	

ALIGNMENTS

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RESULT 1
AAA96336
Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO1899; PRO1890; PRO1887; PRO4785; PRO4353; PRO44357; PRO4405; PRO4356; PRO4352; PRO4380; PRO4354; PRO40408; PRO5737; PRO4425; PRO5990; PRO6030; PRO44352; PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes; insulinemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
                                                                                                                           CDS
                                                                                               sig_peptide
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                         Crohns
                                                                                                                                                                                                                                                                                        cDNA encoding a novel polypeptide designated PRO1484
                                                                                                                                                                                                                                                                                                                  08-FEB-2001 (first entry)
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The present sequence encodes a secreted or transmembrane polypeptide. CC The specification describes polypeptides designated PRO1484, PRO4334, CC PRO1122, PRO1889, PRO1899, PRO1887, PRO1785, PRO4333, PRO4357, PRO4405, CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990, CC PRO6030, PRO4424, PRO4422, PRO4354, PRO4409. PRO1889 polypeptide is CC useful for diagnosing tumour in a mammal. The polypeptides, their CC expression or activity of the polypeptide. Conditions streated include CC obssity, diabetes or hyper-or hypo-insulinemia. The polypeptides are CC capable of inducing proliferation of mammalian kidney mesangial cells CC decreased mesangial cell for treating kidney disorders associated with CC decreased mesangial cell function such as Bergers disease or other CC decreased mesangial cell function such as Bergers disease or other CC decreased mesangial cell function such as Bergers disease or other CC decreased mesangial cell function such as Bergers disease or other CC decreased mesangial cell function such as Bergers disease or other comphropathies associated with Schonlein-Henoch purpura, celiac disease, CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used to generate transgenic animals for use in development and screening of therapeutically useful reagents and also for chromosome identification con the control of the polypeptides and tissue typing.
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                                                                  TTTCCTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACT
 CCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCCAACAATGG
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This sequence represents the cDNA for a human immune system molecule (IMOL) isolated as clone 1890540 from the Incyte BLADTUT07 library.

The human IMOLs (AAB15536-B15550) and their encoding polynucleotides (AAA95775-A95789), and compositions comprising them are useful for the
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TGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCC

Query Match Best Local : Matches 169

Similarity

99.1%;

Score 1696; Pred. No. 0;

DB 21;

Length Indels

Conservative

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Mismatches

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Gaps

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CC The invention relates to the human zacrp3 protein (AAB29580) and to CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue CC of adipocyte complement related protein (ACRP30) and contains a CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a CC terminal Clq domain comprising 10 beta-strands. The zacrp3 gene is CC located on chromosome 5p12. The invention also relates to zacrp3 gene is CC zacrp3-specific antibodies, expression constructs and host cells CC zacrp3-specific antibodies, expression constructs and host cells CC comprising zacrp3 nucleic acids, and methods of recombinant production of CC zacrp3. Human zacrp3, and its agonists and attagonists may be used in the CC study and modulation of cellular metabolism and energy balance in CC mammals, and may therefore be used to treat disorders such as obesity and CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful CC as antimicrobial agents, promoting lysis or phagocytosis of infectious cryanisms such as bacteria or viruses. Zacrp3, its fragments, fusion proteins, antibodies and activity modulators may also be used to inhibit CC collagen-induced platelet aggregation, adhesion, or activation, and may therefore have potential for promoting blood flow within the vasculature CC inserisation and oligomerisation. The present sequence represents cDNA cc encoding human zacrp3 and its antibodies may additionally be used to study considering human zacrp3 and reat injury to the vasculature or other collagenous constructions.
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Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development -
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                                                                                                                             Human; secretory protein; membrane rheumatoid arthritis; diabetes; ss.
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Best Local Similarity 99.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate to cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1709 BP; 480 A; 363 C; 390 G; 476 T; 0 other;
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TGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGT 600
                                                                        AGGGGAGCGGGGCAGCATGGCCCCAAAGGAGAAGGGCTACCCGGGGATTCCACCAGA 420
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                                                                                                                                                    ACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGAT 480
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Pred. No. 0;
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                    ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1692
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γQ	601	GAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 6	60
Db	613	TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACGTCTTCAGCATGTACAGCTA 6	72
Qy	661	GAAATGAAGGGCAAATCAGATACATCCAGCAATC	20
Db		GGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 7	32
Qу	721	CTCCATGGGGACCACCAACGCTTCTC 7	80
Db	733	GATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATGGGGACCACCAACGCTTCTC 7	92
Qy		TGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC 8	40
Db		ACCTTTGCAGGATTCCTGCTCTTTGAAACTAAGTAAATATATGACTAGAATAGCTCCAC	52
7 Q	841	GCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 9	3 8
Ş			
P 09	901	GTTTTACATTGCTGTATTCAAAAAATTATTGGTTCACAATGTTTCACGCTACAGGTACA 	72
γQ	6	CAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1	020
DЬ	973	CCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGA 1	032
Qy	1021	TGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCCTTGGCACCTAAAAGATAAT 1	080
DЪ	1033	ACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAA	092
Qy	1081	TCTCCTCTGACGCAGGTTGGAAATATTTTTTTTTTTCACAGAAGTCATTTGCAAAGAATT 1	140
DЪ	1093	CTCCTCTGACGCAGGTTGGAAATATTTTTTTTTTTATCACAGAAGTCATTTGCAAAGAATT 1	152
Qy	4	TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA	0
Дb		TGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTC	212
Db.	1201 1213	TTATTCTTTATAACATTTGAGAGAATCGGATGTGTGATATGACAGGGCTGGGGCAAGAA 1	260 272
Qy	N	AGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTC	320
DЬ	N	GGCACTAGCTTATTAGCTAATTTAGTGCCCTTCCGTGTTCAGCTTAGCCT	332
Qy	1321	TTTTGATCCACAAAATACATTAAAACTC	380
Db	1333	CCCTTTCCTTTTGATCCACAAAATACATTAAAAACTCTGAATTCACATACAATGCT	392
P 09	1381	TAAAGTCAATAGATTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1	440
Qy	1441	TGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTAT	500
DЪ	1453	ATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTGAGGTTCACTATT 1	512
Qy	1501	AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG	560
Db	Ü	AAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG	572
F &	1561	TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATA	620 632
Qγ		TTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1	680
밁	1633	ATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATATATGGAA 1	692

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RESULT 5
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23-AUG-2000;
30-AUG-2000;
30-SEP-2000;
01-SEP-2000;
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2000US-0189123
2000US-0198123
2000US-020515
2000US-0214886
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2000US-0214889
2000US-0214889
2000US-022963
2000US-0224518
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2000US-0224519
2000US-0225513
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                     and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel human polynucleotides (AAI99513-AAI99538) and the encoded proteins (AAM99915-AAM99934) which are useful for preventing, treating or ameliorating medical conditions e.g. hv protein
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                                                                      ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGCCG
                                                                                                                                                                            AGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAGACTACA
                             <u>ACAAAGGTGACCTGGGGCCTCGAGGGGGAGCGGGGGCATGGCCCCAAAGGAGAAAGG</u>
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29-NOV-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
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Note: The sequence data for this patent did not form part of the specification.
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                                                                                                                                                                                                                                                                                                                                                   Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrob multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1595
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                                                                                                                                                                                                                                                        contraceptive; antiinfertility;
                                                                                                                                                                                                                                                                               haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
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                                                                                                                                     Location/Qualifiers 89..760
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                                                              an protein having specifically is
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claimed in claim 3"
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06-JAN-2000;
11-JAN-2000;
03-FEB-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                     probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate treatment of parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human protein with hydrophobic domain encoding CDNA clone HPIO/81. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA polynucleotides and its complementary sequences may also be used as DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, \, Alzheimer's and inflammation -
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Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection; bacterial infection; fungal infection; diabetes; asthma autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency. Homo sapiens

18-OCT-2001

29-MAR-2001; 2001WO-US10224

06-APR-2000; 2000US-195582F

(GEMY) GENETICS INST

Gulukota K, Wong GG Clark HF, Graham JR; **Fechtel** ~ Agostino Ž, Howes SH, Resnick RJ;

WPI; 2002-179321/23

Five hundred and ninety two polynucleotides human tissue sources which encode secreted preacting immune deficiencies and disorders of the secretary treating immune deficiencies. proteins, useful for such as autoimmune variety for disorders of.

Claim 1; Page 261-262; 372pp; English

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The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also

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GATATGACAGGGCTGGGGCAAGAACAGGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGC
                    GGAACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGT
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XX Human; nool
KW Periphera.
KW Allzheimer
KW Allzheimer
KW Leukaemia.
XX Homo sapii
XX AAI61016-200
XX AUC2001533
XX WO2001533
XX WO20
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25-APR-2000;
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0623450.
2000US-0652450.
2000US-063936.
2000US-0727344.
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Wehrman T, X
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2001-442253/47

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ote: The sequence data for this patent did not form part of the printed
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Local Similarity
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                 AACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGA
                                                                     TGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGA
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93.6%;
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system injuries -
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Pred. No. 0;
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No. 0;
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AAF94076 standard; DNA; 810 ВP

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23-MAY-2001 (first entry)

RESULT 10
AAF94076
ID AAF94
XX AAF94
AC AAF94
XX 23-MAF94
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XX WINDER
DT 23-MAF94
XX Prime
XX Human
XX Fheun
XX Synth
XX Synth
XX EP106 Primer specific for DNA encoding secretory/membrane protein SEQ ij

Human; secretory protein; rheumatoid arthritis; dial diabetes; membrane pabetes; PCR protein; vaccine;

Synthetic

EP1067182-A2

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CC AARB3317 - AABB4419. Included in the invention are primers
CC AARB3317 - AARB4295 and AAR62232 - AAR62325 which are used to isolate the
CC CDNA sequences of the invention. The invention also includes methods for
CC the production of antibodies directed against the proteins, and cDNA
CC sequences, which can be used in vaccines. The polynucleotide sequences
CC can be used in gene therapy. The polynucleotide sequences and the
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with inappropriate secretory
CC sequences may also be used as DNA probes in diagnostic assays
CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
CC presence of similar nucleic acid sequences in samples. They may also be
CC used to study the expression and function of secretory proteins/membrane
CC polypeptides and their role in metabolism. The polypeptides may be used
CC agents to down regulate supersists and antagonists of expression and
CC activity. The antibodies and antagonists may also be used as therapeutic
CC agents to down regulate expression and activity. The antibodies may also
De used as diagnostic agents for detecting the presence of the
CC polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                          Matches
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides in samples (e.g. (ELISA). Examples of diseases arthritis and diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                    810 BP;
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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or as candidate target molecules in drug development
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smatches 7;
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                                                                                       Agarwal P, Smith RF,
                                                                                                                                                           (SMIK )
(SMIK )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; membrane-associated protein; hypertension; inflammatory disorder; neurological disorder; haematopoietic disorder skeletal developmental disorder; growth abnormality; autoimmune disorder neurodegenerative disorder; nervous system disorder; bacterial infeperipheral myelinopathy; viral infection; cancer; obesity; diabetes hypotension; sexual development disorder; blood disorder; gene; ds.
                        WPI; 2002-188468/24.
P-PSDB; AAU84371.
                                                                                                                                                                                                                                                        12-JUL-2000;
21-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK35591;
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Matches 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel sec
encoding
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                                                                                                                                                    CATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCATTC
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                                                                                                                                                 The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.
                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide used in the identification disorders and encoding polypeptides used for treating i disease, cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory
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                                                                                             ABL34928
                                Rat cDNA isolated from skin cells
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                                                                                                                                                             AGAATCAACCACAAAATAGTCTTCTCAGA 1020
                                                                                                                                                                                      AGTAAATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGGGCT-GATTTG
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                                                                                                                                                 AGAATAGACCACAAGGTAATATTCCCAGA 1035
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                                                                                                                                                                                                                                                                           AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG
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                                                                                              standard;
                                                                                              cDNA;
                                                   entry!
                                                                                              1035
                                SEQ ID NO: 424.
          cancer;
incer; growth defect;
dermatological; vulnerary;
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Watson
                                                                                                                24-MAY-2000;
25-JUL-2000;
                                                                                                                              24-MAY-2001;
                                                                                                                                       29-NOV-2001.
                                                                                                                                                WO200190357-A1
                                                                                                                                                                   immunomodulator; anti-inflammatory; cytostatic; neuroprotective;
ss.
                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD
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                                                                                                                2000US-206650P
2000US-221232P
                                                                                                                              2001WO-NZ00099
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                                                                                              Onrust R,
                                                                                              Murison
                                                                                              JG,
                                                                                              Kumble
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New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for modulating immune responses

2002-122020/16

Claim 1; Page 262; 466pp; English.

The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound have important modulating immune responses. The present sequence is a invention

Sequence 1035 BP; 255 A; 242 Ç; 298 G; 240 T; 0 other;

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Query Match
Best Local Sin
Matches 819;
Similarity 82.8
19; Conservative
          40.7%;
82.8%;
 0;
          Score 696.2;
Pred. No. 5.1
  Mismatches
           . 1e-]
                  DB 24;
                  Length
                   1035
 2;
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] -	Qy	Db	Оу
	93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGTGTAAGATGAAT 152	48 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC 107	33 CTCTGCTGTCTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGCAGC 92
167	152	107	92

168	153
	153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212
?7	N

U	`
228 A	213
TTATGGA	213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272
37	72

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DЬ	Qy
348	333
348 AAGGAGACAAAGGCGACCTGGGGCCTCGAGGGGAACGGGGGCAGCATGGCCCCAAAGGAT 407	333 AGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGAGCGGGGGGGAGCATGGCCCCAAAGGAG 392
407	392

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453

CCCACTTCAGCAATCAGAACAGTGGGAATTATCTTCAGCAGTGTTGAGACCAACATTGGAA

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RESULT 14
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        WPI; 2000-072177/06
                                                                       29-APR-1998;
09-NOV-1998;
                                                                                                                          04-NOV-1999
                                                                                                                                               W09955865-A1
                                                                                                                                                                                       anti-inflammatory;
                                                                                                                                                                                                                                                              cDNA encoding
                                                                                                                                                                                                                                                                                                                              AAZ61633 standard;
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                                                                                                     29-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                 AGAATAGACCACAAGGTAATATTCCCAGA 1035
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                             Sleeman
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                              rat skin cell secreted protein,
                                                                      98US-0069726
98US-0188930
                                                                                                     99WO-NZ00051
                                                  RES
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                                                  & DEV CORP LTD
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                             Watson
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dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, cc and mouse embryonic skin, keratinocyte stem cells and transit amplifying cc cells. Polypeptides of the invention may be used to treat inflammation, cc cancer and neurological diseases. The proteins may be used to stimulate cc the growth and motility of keratinocytes, to inhibit the growth of cc cancer cells, to modulate angiogenesis and tumour vascularisation, to codulate skin inflammation, to modulate epithelial cell growth and to cc inhibit binding of HIV-1 to leukocytes. The invention may also be used cc inhibit binding of HIV-1 to leukocytes. The invention may also be used cc disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived cc from several mouse, rat or human skin cell types. Sequences Cc AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode cc proteins with an N-terminal signal sequence, indicating that the proteins can daAZ61827-Z61839 encode proteins with one or more putative Novel polynucleotides useful for including wounds and cancer -Claim 1; Page relates 235pp; to novel nucleic acid sequences derived from rat keratinocytes and neonatal foreskin fibroblasts English. the treatment of various conditions

Sequence 1123 BP; 277 A; 266 C; 321 G; 258 T; 1 other;

transmembrane domains.

Query Match Best Local S

40.7%;

21;

Length

2:

밁 밁 ρy 망 δõ 밁 δÃ δÃ δõ δÃ DЬ δÃ В δÃ Вþ Š 밁 δ Š 밁 밁 Matches 616 513 556 453 496 393 436 333 376 273 316 213 256 153 196 136 93 ω CCTTCAGCATGAAGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG TCATCTATTGGCAACTGCTTGGCTTTTTTTCCTCCCTTTTTGCCTGTGTCAAGATGAAT 152 CCCATCAGCTTCCCCGGGGAGATTCTGCCGATTTGTCACGAGCCATGCTCAGGAGGCAGC CTCTGCTGTCTTCTCAGGGAGACTCTGAGGCTCTGTTGAGAATCATGCTTTTGGAGGCAGC eal Similarity 819; Conserv GCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGATACATCCAGCA ACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGGTGTGTATTTCTTCA 572 CCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCCAACATTGGAA 512 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332 ATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGTCCTCCTGGCATTCCAG ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG TCGTCTGGTGGCACCTGCTGGCTTTGCTTTTCCTCCCATTTTGCCTGTGTCAAGATGAAT ACTTCTTCGATGTCATGACTGGTAGATTTGGGGGCCCCCGTATCAGGCGTGTATTTCTTCA CTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTTGAGACCAACATTGGAA ACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCCACCGGGCCCTCCTGGCATTCCAG ACATGGAGTCTCCACAAGCTGGAGGACTGCCCCCAGACTGCAGCAAGTGTTGCCATGGAG Conservative 0; Score 696.2; DB 21; Pred. No. 5.3e-192; 0; Mismatches 168; Indels 2: Gaps 435 195 615 555 452 375 315 632 675 272 212

736

GTAACACGGTGTTCAGCATGTACAGCTATGAAACAAAGGGAAAATCAGATACATCCAGCA

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RESULT 15
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The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifyin cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to
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09-NOV-1998;
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                                                                                                                                                                                                                               Sleeman
                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour vascularisation; growth disorder;
disorder; skin wound; hair follicle disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1123 BP;
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                                                                                           CTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTGAAACTA
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                                        AGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCT-GATTTG
                                                                              CCCTCCATGGGGACCACCAGCGCTTCTCTACCTTCGCAGGCTTTCTGCTTTTTGAAACTA
                                                                                                                                  ACCATGCAGTGCTGAAGTTGGCCAAAGGAGATGAAGTCTGGCTAAGAATGGGCAACGGTG
                                                                                                                                                ATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGCCAATGGCC
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                          AGTGATGAGGAAGTCAGGATAGCTCCATGCTAAGGGCGATTTGTAGGTGAGCTAGGGTTG
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No. 5.3e-192;
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Maximum DB
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               GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
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10 US-09-864-761-12152

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10 US-10-046-935-1716

10 US-09-878-178-1716

10 US-09-854-133-151

10 US-09-776-976-5
           0 US-09-758-055-5

0 US-09-909-47-5

0 US-09-964-824A-235

0 US-09-776-976-3

0 US-09-758-055-3

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US-10-040-739-1335
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US-10-035-855-1
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(without alignments)
5917.260 Million cell updates/sec
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Sequence 1716, Ap
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Sequence 12152, A
Sequence 28732, A
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PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR APPLICATION NUMBER: 60/114140
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
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APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication No.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C8
CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR APPLICATION NUMBER: 60/085579
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR FILING DATE: 1998-12-15
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                                                                           PRIOR APPLICATION NUMBER: 60/116843 PRIOR FILING DATE: 1999-01-22
                                                                                                                              PRIOR APPLICATION NUMBER: 60/115552 PRIOR FILING DATE: 1999-01-12
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                        APPLICATION NUMBER: 60/125774 FILING DATE: 1999-03-23
APPLICATION NUMBER: 60/125778
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OR FILING DATE: 1999-05-04
OR APPLICATION NUMBER: 60/132379
OR FILING DATE: 1999-05-04
OR APPLICATION NUMBER: 60/132383
OR FILING DATE: 1999-05-26
OR APPLICATION NUMBER: 60/135750
OR FILING DATE: 1999-05-25
OR APPLICATION NUMBER: 60/138166
OR FILING DATE: 1999-07-20
OR FILING DATE: 1999-07-20
OR APPLICATION NUMBER: 60/146970
OR APPLICATION NUMBER: 60/162506
OR FILING DATE: 1999-10-29
OR APPLICATION NUMBER: 1999-10-29
OR APPLICATION NUMBER: 09/311832
OR FILING DATE: 1999-08-10-29
OR APPLICATION NUMBER: 09/311832
OR FILING DATE: 1999-08-25
OR APPLICATION NUMBER: 09/34042
OR APPLICATION NUMBER: 09/444848
OR APPLICATION NUMBER: 09/747259
OR APPLICATION NUMBER: 09/816744

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DR FILING DATE: 1990-03-31
DR FILING DATE: 1990-04-05
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OR FILING DATE: 2001-02-28
OR APPLICATION NUMBER: PCT/US01/17800
OR FILING DATE: 2001-06-01
OR APPLICATION NUMBER: PCT/US01/19692
OR FILING DATE: 2001-06-20
OR APPLICATION NUMBER: PCT/US01/21066
OR APPLICATION NUMBER: PCT/US01/21735
OR FILING DATE: 2001-07-09
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2000-06-02

NUMBER: PCT/US00/23522 : 2000-08-23

NUMBER: PCT/US00/14042 : 2000-05-22 NUMBER: PCT/US00/05841: 2000-03-02

PCT/US00/15264

NUMBER: PCT/US00/32678: 2000-12-01

NUMBER: PCT, : 2000-08-24

PCT/US00/23328

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OR FILING DATE: 2001-03-22
OR APPLICATION NUMBER: 09/854208
OR FILING DATE: 2001-05-10
OR APPLICATION NUMBER: 09/854280
OR FILING DATE: 2001-05-10
OR APPLICATION NUMBER: 09/874503
OR FILING DATE: 2001-06-29
OR APPLICATION NUMBER: 09/908,827
OR FILING DATE: 2001-07-18
OR FILING DATE: 2001-07-18
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OR APPLICATION NUMBER: PCT/US99/30720
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RESULT 2
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; Sequence 1, Application US/10035855
; Publication NO. US20030008348A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

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; NUMBER OF SEQ ID NO 1
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FILING DATE: 1999-05-14
APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/30720
FILING DATE: 1999-12-22
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FILING DATE: 2000-12-20
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: 2001-02-28
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APPLICATION NUMBER: 09/854208
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PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILLING DATE: 1998-05-15

PRIOR FILLING DATE: 1998-12-15

PRIOR FILLING DATE: 1998-12-15

PRIOR APPLICATION NUMBER: 60/113300

PRIOR FILLING DATE: 1998-12-22

PRIOR PRIOR FILLING DATE: 1998-12-23

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PRIOR FILLING DATE: 1998-12-23

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PRIOR PRIOR
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APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audre
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CURRENT FILING DATE: 2001-12-26
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                                                                                             DR APPLICATION NUMBER: 60/11552
DR FILING DATE: 1999-01-12
DR APPLICATION NUMBER: 60/116843
DR FILING DATE: 1999-01-22
DR APPLICATION NUMBER: 60/125774
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OR FILING DATE: 2001-06-01
OR APPLICATION NUMBER: PCT/US01/19692
OR FILING DATE: 2001-06-20
OR APPLICATION NUMBER: PCT/US01/21066
OR FILING DATE: 2001-06-29
OR APPLICATION NUMBER: PCT/US01/21735
OR FILING DATE: 2001-07-09
OR FILING DATE: 2001-07-09
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US-09-822-849A-359

Sequence 359, Application Patent No. US20020045170A1 GENERAL INFORMATION:

US/09822849F

APPLICANT: Wong, Gordon G APPLICANT: Clark, Hilary APPLICANT: Fechtel, Kim APPLICANT: Agostino, Micl APPLICANT: Howes, Steven

Fechtel, Kim Agostino, Michael Howes, Steven H.

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Best Local S
Matches 1365
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LENGTH: 1608
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
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TYPE: DNA
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                                           AATGTTGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAAT
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            TTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT
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TTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT
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Graham, James R.
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                                                               Sequence 12152, Application Patent No. US20020048763Al GENERAL INFORMATION:
      TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                  APPLICANT:
                                                    APPLICANT: Penn, Sharron
FILE REFERENCE: Aeomica-X-1
                          APPLICANT:
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                         Rank, David R.
Hanzel, David K
Chen, Wensheng
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: ACOMIGA-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669

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                                                                                                                                                                                                                                                                                              Patent No. US2002004
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                      CURRENT APPLICATION NUMBER: US/09/864,761 CURRENT FILING DATE: 2001-05-23 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03 PRIOR APPLICATION NUMBER: GB 24263.6
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                                                                                                                                                                    FILE REFERENCE:
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ORGANISM: Homo sapiens
FEATURE:
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5. US20020048763A1
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EXPRESSED IN BONE I
EXPRESSED IN LUNG,
EXPRESSED IN ADULT
EXPRESSED IN BRAIN
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IN LUNG, SIGNAL = 1.1
IN ADULT LIVER, SIGNAL = 1.4
IN BRAIN, SIGNAL = 0.82
IN PLACENTA, SIGNAL = 1.1
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Pred. No. 4.4e-28;
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                                                    GENERAL INFORMATION:
                                                                       Sequence 1716, Application Patent No. US20020156011A1
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, 9
APPLICANT: Secrist, Hea
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-864-761-28732
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Best Local
                                                                                                                                                                                                Matches
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NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION:
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TYPE: DNA
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                                                                                 AGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCC 547
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                                                                                                                                                                                              7.6%; Score 130; DB 10; larity 100.0%; Pred. No. 9.5e-27; Conservative 0; Mismatches 0;
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NN: EXPRESSED IN BONE MARROW, SIGNAL = 0.83

NN: EXPRESSED IN LUNG, SIGNAL = 1.1

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

NN: EXPRESSED IN BRAIN, SIGNAL = 0.82

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.1

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96

NN: NT HIT: U29581.1, EVALUE 2.90e-01

NN: SMISSPROT HIT: P98087, EVALUE 2.70e-01

NN: EST_HUMAN HIT: AA334609.1, EVALUE 2.00e-67
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NUMBER: US 09/608,408
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Secrist, Heather

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                                                                                                                                               ; ORGANISM: Homo sapien US-09-878-178-1716
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TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1716
LENGTH: 432
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FAST-SEQ for Windows Version 4.0
SEQ ID NO 1716
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Best Local Similarity 52.4%;
Matches 173; Conservative
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                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                             APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
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TYPE: DNA
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                                                                     y Match 4.6%; Local Similarity 52.4%; hes 173; Conservative
 89
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 ATTGTGTTTGATCTTCTGCACCAACATTAGGAGAAACTTTTGATCTTCAGCTTGGTAGA 148
                     ATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGA 538
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Stolk, John A.
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Pred. No. 3.8e-12;
0; Mismatches 157;
                                                                     Score 78.8; DB 9;
Pred. No. 3.8e-12;
0; Mismatches 157;
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; TYPE: DNA ; ORGANISM: Homo sapien US-09-854-133-151
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 151
LENGTH: 3275
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Best Local Similarity
Matches 173; Conserv
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CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
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52.4%;
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Pred. No. 1.4e-11;
0; Mismatches 157;
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TYPE: DNA
ORGANISM: Homo sapien
US-09-738-973-151
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US-09-738-973-151
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                                                                                                                                                                                    Sequence 5, Application US/09776976 Patent No. US20020037849A1
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Best Local Similarity
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                                                        APPLICANT: Fruebis, Joachim
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
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CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
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CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
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Kalos, Michael D.
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Indirias, Carol Yoseph
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Pred. No. 1.4e-11
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SEQ ID NO 5

ORGANISM: Homo sapiens

TYPE: DNA

ENGTH: 4517

SOFTWARE:

Patent.pm

NUMBER OF SEQ ID NOS:

PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13

CURRENT APPLICATION NUMBER: US/09/758,055

PRIOR APPLICATION NUMBER: US 60/299,881 PRIOR FILING DATE: 2000-09-01

APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG

APPLICANT: APPLICANT: APPLICANT:

APPLICANT: Fruebis, Joachim

Yen, Frances

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                                                             US-09-758-055-5
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GENERAL INFORMATION:
                  Sequence 5, Application US/09758055 Patent No. US20020058617A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patent.pm
SEQ ID NO 5
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PRIOR APPLICATION NUMBER: US-60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US-60/198,087
PRIOR TILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US-60/299,881
PRIOR FILING DATE: 2000-09-01
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Pred. No. 2.5e-10;
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                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                               SEQ ID NO 5
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PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
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CURRENT FILING DATE: 2001-07-19
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PRIOR FILING DATE: 2001-02-05
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RESULT 14
US-09-964-824A-235
; Sequence 235, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
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Best Local Similarity 50.48;
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                                                        GAGAACCTGGAGAAGGTGCCTATGTATACCGCTCAGCATTCAGTGTGGGATTGGAGACTT
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Pred. No. 2.5e-10;
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SOFTWARE: Patent.pm
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 1276
TYPE: DNA
ORGANISM: mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILLING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILLING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILLING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
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                                                                           ATTATGACGGCAGCACTGGCAAGTTCTACTGCAACATTCCGGGGACTCTACTACTTCTCTT
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Search completed: January 15, 2003, 19:35:51 Job time: 144 secs

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SUMMARIES

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ALIGNMENT

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF326976	RESULT 1
of the human CORS26 gene	Maeda, T., Hayashi, A. and Saito, T.	1 (bases 1 to 1730)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens.	•	AF326976.1 GI:14586742	AF326976	Homo sapiens putative secretory protein CORS26 mRNA, complete cds.	AF326976 1730 bp mRNA linear PRI 03-JUL-2001		

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JOURNAL REFERENCE
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TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA
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321 ATTTTGACCTGGCTTTÆGATAAAACTGTGGCAAGAAAATGTAATGAGCAATATATGGAA 16 	Qу 16 Db 16	
561 TTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAATAACCTTTAGAGAAAG 16 	Qy 15 Db 15	
O1 AACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAAATGTTGCATG ! 	Qy 15 Db 15	
41 ATGTTCCCCCACATCGCCCCAACTTCGGATGTGGGGTCAGGAGGTTCAGGTTCACTATT 1		
81 TAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGGTTGTAATTTTGTGT 1 	Qy 13 Db 13	
21 ACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTCACATACAATGCTATTT 13	Qy 13 Db 13	
61 CAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCGTGTTCAGCTTAGCCTTTG 132	Qy 12 pb 12	
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41 TTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGTTTTAAGTTCA 120 	11	
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01 GTTTTACATTGCTGTATTCAAAAAATTÄTTGGTTGCAATGTTGTTCACGCTACAGGTACA 960 	Qy 91	
1 TTTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGG 9	Qy 84 Db 84	
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1 TGAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGG 720 	Oy 66	
1 TGAGGAAGTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTA 66	Db 60	

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GVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEV
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1696; CONSETVATIVE GCCCGAGGAGACCACGCTCCTGG	protein* /protein_id="AAK17961.1" /protein_id="AAK17961.1" /db_xref="GI:13274520" /db_xref="GI:13274520" /translation="MLWRQLIYWQLLALFFLPFCLCQDEYMESPOTGGLPPDCSKC /translation="MLWRQLIYWQLLALFFLPFCLCQDEYMESPOTGGLPPDCSKC /translation="MLWRQLIYWQLALFFCHEGAKGEKGDKGDLGPRGERGG GYSFRGYGGPPGPPGPPGPHGNHGNNGNGATGHEGAKGEKGDKGDLGPRGERGG PKGEKGYPGIPPELQIAFWASLATHFSNQNSGIIFSSVETNIGNFTDVMTGRFGRAG PKGEKGYPGIPPELQIAFWASLATHFSNQNSGIIFSSVETNIGNFTDVMTGRFGRAG GYUFFTESDMKHEDVESYYVYLAHLNGNTYFSMYSYEMKGKSDTSSNHAVLKLAKGD WLRMGNGALHGDHQRFSTFAGFLLFETK* 484 a 358 c 392 g 476 t 484 a 358 c 392 g 476 t tch 99.1%; Score 1696; DB 9; Length 1710; tch 100.0%; Pred. NO. 0;	/db_xrei="taxon /chromosome="5" /map="5p13-p12" 11710 /gene="CTRP3" /note="2ACRP3" /note="CTRP3" /gene="CTRP3" /gene="CTRP3" /product="comp10"	Homo Saplens Unpublished 2 (bases 1 t Piddington,C. Direct Submis Submitted (20 Eastlake Ave. Loca 1. 2e /org	AF329837.1 GI:13274519 AF329837.1 GI:13274519 Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1710) Piddington, C.S. and Bishop, Primates; Catarrhini; Factor related protections.	AC CI
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Patent: EP 1067182-A 261 10-JAN-2001;
Helix Research Institute (JP)
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                                                                                                                                      GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA 960
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                          GTTTTACATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACA
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1927)
Kato,S. and Kimura,T.
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DKGDLGPRGERGQHGPKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIG
NFLMS*
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AACCCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGA
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                                                                                                                                                                                                                                      Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                Strausberg, R.
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              Series: IRAL Plate: 38 Row: p
                             through the I.M.A.G.
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Mammalia; Eutheria; Primates;
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                                            distribution:
Location/Qualifiers
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             MGC clone distribution
.E. Consortium/LLNL at:
38 Row: p Column: 18.
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                             information can be http://image.llnl
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Best Local Similarity 99.9
Matches 1284; Conservative
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/db_xref="G1:16359109"
/tanslation="MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRRGAPVSGVYF
FTFSMKKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAEGDEVWLRM
GNGALHGDHQRFSTFAGFLLFETK"
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/tissue_type="Placenta"
/clone_lib="NHH_MGC_79"
/lab_host="DH10B"
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factor-related protein; likely ortholog of mouse Containing sequence of 26-kDa
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/db_xref="taxon:9606"
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                                  Direct Submission
Submitted (07-MAR-2002) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
On Mar 7, 2002 this sequence version replaced
-------Genome Center
                                                                               Direct Submission
Submitted (23-MAR-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 155013)
DOE Joint Genome Institute.
 Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gu
                                                                                                                                                                                Mammalia; Eutheria; Primate
1 (bases 1 to 155013)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                HTG;
                                                                                                                                       DOE Joint Genome Institute.
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AC026707
AC026707.5 GI:19
                                                                                                                                                                                                                                                                                        AC026707 155013 bp
Homo sapiens chromosome 5 clone
                                                                                                                                                            Unpublished
                                                                                                                                                                      Sequencing of Human Chromosome
                                                                                                                                                                                                                             Homo
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HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
http://www.jgi.doe
                                                                                                                                                                                                      Primates;
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Creek, CA !
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Query Match
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GCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTCAGGAACCCCTGAAGT
                                                          TACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAG
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Consensus quality: 154674 bases at least 030
Consensus quality: 154871 bases at least 020
Estimated insert size: 171000; pulse field gel estimation
Estimated insert size: 154913; sum-of-contigs estimation
Quality coverage: 9.64 in 020 bases; sum-of-contigs estimation
Quality coverage: 10.64 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs-of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
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Center Project Name: 656404
Center clone name: CITB-H1_
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This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved. 6677: contig of 6677 bp in 16678 677: gap of unknown length 6778 155013: contig of 148236 bp in
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Submitted (03-AUG-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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SHGC-56588 G36925
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Pred. No. 8e-254;
0; Mismatches
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                            AGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGGGGGACAAAGGTGACCTGGGGCCTCG
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Sequence 51(
AX136588
AX136588.1
                                                                                                                                                                                                                                                                                                                                             Secretory protein or membrane protein
Patent: EP 1067182-A 510 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       Ota,T., Isogai,T., Nishikawa,T., Kawai,Y.,
Hayashi,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/db_xref="taxon:9606"
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98.9%;
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Pred. No. 3.4e-183;
Pred. No. 3.4e-183;
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EP1067182.
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GAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTTCCTCCCTT 131 GAGCCATGCTCGGGAGGCAGCGCATCTGGTGGCACCTGCTGCCTTTGCTTTTCCTCCCAT 165

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1 (bases 1 to 1117)
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                         Similarity
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                                                                                                                                                                  /codon_start=1
/protein_id="CAC16633.1"
/brotein_id="CAC16633.1"
/db_xref="GI:11229977"
/db_xref="GI:1122997"
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/db_xref="taxon:10090"
1111. .851
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272 c 293 g 268 t
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Eutheria; Rodentia;
                       40.6%;
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Score 695.8; DB
Pred. No. 3e-165;
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Murinae; Mus
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Maeda,T., Abe,M., Kurisu,K., Jikko,A. a
Molecular cloning and characterization
encoding a putative secretory protein a
in skeletal development
J. Biol. Chem. 276 (5), 3628-3634 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAR-2000) Radiology and Radiation University School of Dentistry, 1-8 Yamadaoka, 9565-0871, Japan
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Direct Submission
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                                                                                                                      ATGYTNTGGMGNCARYTNATHTAYTGGCARYTNYTNGCNYTNTTYTTYYTNCCNTTYTGY
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                                     al Similarity
526; Conserv
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AX136727
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                                                                                                                                                                           Mammalia; Eutheria; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 552)
Ota, T. Tennai m
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                                     Conservative
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                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
105 c 101 g 17
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                                     Score 498.6; DB 6;
Pred. No. 2.6e-115;
0; Mismatches 15;
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EP1067182.
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ATTTGAGAGAATCGGATGTAGTGATATGACAGGGGCTGGGGCAAGAACAGGGGGCACTAGCT 1274

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                       ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG
                                              GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAAACC
                                                                                                                                                                                                           proteins
Patent: WO 0149728-A 49 12-JUL-2001;
Protegene Inc. (JP) ; SAGAMI CHEMICAL
Location/Qualifiers
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalla; Eutheria; Primates; Catarrhini;
1 (bases 1 to 672)
Kato, S. and Kimura, T.
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Sequence 49 from Patent W00149728.
AXI91527
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/db_xref="taxon:9606"
170 c 187 g 13
                                                                                                                           21.1%; Score 361; DB 6; 100.0%; Pred. No. 1.9e-80;
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Job time

Search completed: January 15, Job time: 4496 secs

2003, 18:56:35

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RESULT 15
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                                          ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCC
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                                                                                  GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC
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                                                                                                                                                                       1 Similarity 99.5
208; Conservative
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Baker, K.P., Goddard, A. and Wood, W.I.
                                                                                                                                                                                                                                                                               Genentech,
                                                                                                                                                                                                                                                                                      Human polypeptides and methods for th Patent: WO 0107611-A 240 01-FEB-2001;
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 546)
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/db_xref="taxon:9606"
129 c 155 g 10
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Pred. No. 1.1e-41;
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1712
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RESULT 1
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SOURCE COMMENT REFERENCE FEATURES JOURNAL MEDLINE TITLE ORGANISM AUTHORS Athersys, Inc. 3201 Carnegie Ave, (Tel: 216 431 9900 Fax: 216 361 9596 ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 776)
Harrington, J.J.; Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith F. Veloso N. Kilvan, Hose T. Othern K. 10 K. Offenhaber RST5388 Athersys RAGE Library Homo BG186424 BG186424.1 GI:13708111 Contact: Scott J. Cain Homo sapiens BG186424 21227151 human. 1: scain@athersys.com quality sequence stop: 498. Location/Qualifiers Cleveland, 776 bp 유 44115, mRNA sapiens cDNA, mRNA sequence. USA linear EST 21-APR-2001

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Best Local Similarity Matches 421 361 301 241 181 809 121 548 488 481 908 728 61 \vdash CCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAA 607 ATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTC 487 GTGTATGTGTACCTTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATG 667 AGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGGCC ATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTC 60 GACTAATATACTCAGCATCTTTATCACTCTTTCCTTGGCACCTAAAAGATAATTCTCCTC TGTTGGACAATTCAGGGGCTCAGAAGAATCAACCACAAAATAGTCTTCTCAGATGACCTT ATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAA ATTGCTGTATTCAAAAAATTATTGGTTGCAATGTTGTTCACGCTACAGGTACACCAATAA AAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTAC AAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTAC GTGTATGTGTACCTTATGCACAATGGCGACACAGTCTTCAGCATGTACAGCTATGAAATG CCAGTATCAGGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAA 180 AGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCC 547 220 Conservative /note="see 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances." /organism="Homo sapiens"
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RESULT 2 BG186928/c

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1 (bases 1 to 874)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001) Tel: 216 431 9900 Fax: 216 361 9596 Athersys, Inc. 3201 Carnegie Ave, Contact: Scott J. Cain BG186928.1 RST5905 Athersys RAGE Library Homo Similarity l: scain@athersys.com
quality sequence stop: Conservative a Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances." /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Location/Qualifiers /organism="Homo sapiens" 43.4**%**; 94.7**%**; Cleveland, Score 743.4; Pred. No. 2.8e 0; Mismatches 0; 874 bp Н DB 12; 2.8e-172; 44115, USA sapiens mRNA cDNA, mRNA sequence linear Length EST 4; Gaps 440 560 620 680 ω

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                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12807 row: f column: 13
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                                                                                                                                                                                                                                                     Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
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Location/Qualifiers
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   CCAGTATCAGGTGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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quality sequence stop: 504.
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Athersys RAGE Library
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/db_xref="taxon:9606"
/clone_lib="Athersy" RAGE Library"
/cell_line="HT1080"
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Plate: LLCM1331 row: h column:
                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG400260
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                                                                                                                                                                                                                                             quality sequence stop:
Location/Qualifiers
/clone="IMAGE:4592701"
/clone=lib="NIH_MCC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); S' and
SiI (ggccgctcggcc); Site_2: SiI (ggccattatggcc); S' and
3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGACGCGCCGACATG-GT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                              /organism="Homo sapiens"
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Consortium/LLNL

(LLNL) can

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                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CAGCAGTGTTGAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGC
                                      GCGGGGGCAGCATGGCCCCAAAGGAGAGAGAGGGCTACCCGGGGATTCCACCAGAACTTCA 426
                                                                                                                                                     TGGTCATGAAGGAGCCAAAGGTGAGAAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGA 366
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                                                                                                                                                                                          GCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCAC
                                                                GATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTT
                                                                                          GCGGGGGCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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1 (bases 1 to 815)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed) upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Not this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:5199982"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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RST22308 Ath
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BG202940.1
EST.
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Athersys, Inc.
3201 Carnegie Ave, Cleveland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                                                                                                                                                                                         Tel: 216 431 9900
Fax: 216 361 9596
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                                                                                         256
                                                                                                                                                                                                                                                                                                    quality sequence stop: 542.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     scain@athersys.com
                                                                                         a
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Athersys RAGE Library F
                                                                                    Libraries using Random Activation of Gene Expression, Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                          /note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                              /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                  38.0%;
97.2%;
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LOCUS

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RST24381 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

RCESSION

BG204962

VERSION

BG204962.1 GI:13726649

REYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 773)

AUTHORS

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher JOURNAL

MEDLINE

Creation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

COMMENT

Athersys, Inc.

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                             TCTGACCCAGGTTGGAA -- ATTTTTTTTTATTACAGAAGCCATTGGCAAAGAATTTGACT
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Tel: 216 431 9900
Fax: 216 361 9596
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/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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BQ637986.1 G
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Plate: 17 row: a column:
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Contact: Wistow G
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 770)
Harrington, J. J., Sherf, B., Rur
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BG195757
EST.
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                                                                                                                                                                                                                                                                                      Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
                                                                                                                                                                                                    Contact: Scott
Athersys, Inc.
                                                                                                                                                                                                                                                                          ,E.,
                                                                                                                                                              1 Carnegie Ave,
216 431 9900
216 361 9596
                                                                                                                           l: scain@athersys.com
quality sequence stop:
    Location/Qualifiers
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Danzig, J. and Ducar, M.
                                                                                                                                                                                                                Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                          770 bp
Athersys RAGE Library I
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily
                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 818)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,Cain,S., Leventhal,C., McElligott,K., Boozer,S., Mays,R., Smitl, Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smitl, Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher

DEFINITION ACCESSION

BG183776 RST2684 Athersys BG183776 BG183776.1 GI:13

RAGE Library

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 GTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA 1550
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Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
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/cell_line="HT1080"
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BM819819
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Fax: +82-42-860-4409
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Contact: Kim YS
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e: 17 row: A column: 08
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    S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
    Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

                                                                                                                                                                                                                                                                                                                                                                                  /note-*organ: Stomach: Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand course of the coll was trand the day of the coll was tranded by the coll was tranded to the co
                                                                                                                                                                    converted to a DNA strand by Okayama Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF by electroporation method The cDNA libraries constructed by this method are full-length enriched cDNA library."
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                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AA527298
AA527298.1 GI
                                      CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1007 Std Error: 0.00
Stg primer: -00ml3 fwd. ET from Amersham
                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, F
Email: cgapbs-remail.nih.gov
Tissue Procurement: Elias Can
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 594)
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ng39h03.s1 NCI_CGAP_Co3
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                    quality sequence stop: 473.
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Homo
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Catarrhini; Hominidae
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                                                                             AACATACACTATTAATAAATACCTTAGAGAAAGATTTTGACCTGGCTTTAGATAAAACTG
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TGGCAAGAAAATGTAATGAGCAATATATGGAAATAAACACACCTTTGTTAAAG
                                                                                                                              GTACAGTGCCAATAGATATTCAAATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   normalization.
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/tissue_type="colon"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 1.7e-135;
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mRNA sequence. BG571867 BG571867.1 GI EST.

BG571867 794 bp n 602593213F1 NIH_MGC_79 Homo sapiens

CDNA

linear EST 10-A clone IMAGE:4720611

10-APR-2001

Homo

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                  TTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGG 901
                                                                                                                                    GAAATGAAGGGCAAATCAGATACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGG
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 TTGGGGAAGACTTGTAGCTGAGCTGATTTGTTACGATCTGAGGAACATTAAAGTTGAGGG
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High quality sequence stop: 760.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc); S' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ACTGCTATATGGCC-3' and 3' adaptor sequence: 5'-ACTGCTAGAGCCGACATG-GTG-GT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="INAGE:4720611"
/clone_lib="NIH_MGC_79"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium Unpublished (2000)

Contact: Douglas Welton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI964101 555 bp mRNA linear EST 12-MAR-2: 1664H09:y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5671913 5' similar to SW:CERL_RAT P98087 CEREBELLIN-LIKE GLYCOPROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available consortium, for clone orders contact: info@image.llr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
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1 (bases 1 to 555)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 429.
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library
                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                               /clone_lib="Melton Normalized Human
                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5671913"
                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                           /dev_stage="Adult"
                                                                                                                                                                                                                                                  /tissue_type="Islets
                                                                                                                                                                                                                                                                            /sex="Both"
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     of Langerhans"
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Blistain, A.,
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                     AAGTCATTTGCAAAG 1136
                                                                                                  ACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCC 1061
                                                                                                                                               TGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAAGAATCAACC 1001
                                                                                                                                                                            TGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGGCAATGGCGCTCTCCATG 761
                                           ACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCACTCTTTCC
                                                                                                                                   TGTTCACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGGCTCAGAAGAATCAACC
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Search completed: January 15, 2003, 19:31:52 Job time: 2259 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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   US-09-188-930-28
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US-08-463-911-6
US-09-140-804-9
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US-08-949-795-1
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US-09-336-33-744-1
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Qy 333 AGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGGAGCATGGCCCCAAAAGGAG 392	Qy 273 GAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGA 332 	OY 213 ACTACAGCTTTCGAGGCTACCAAGGCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAG 272	Oy 153 ACATGGAGTCTCCACAAACCGGAGGACTACCCCCAGACTGCAGTAAGTGTTGTCATGGAG 212	Qy 93 TCATCTATTGGCAACTGCTGGCTTTGTTTTTCCTCCCTTTTTGCCTGTGAAGATGAAF 152	Qy 33 CTCTGCTGTCTTCTCAGGGAACTCTGAGGCTCTGTTGAGAATCATGCTTTGGAGGGCAGC 92	Query Match 40.7%; Score 696.2; DB 3; Length 1123; Best Local Similarity 82.8%; Pred. No. 3e-195; Matches 819; Conservative 0; Mismatches 168; Indels 2; Gaps 2	33 53 3.1 1416 1 US-07-621-0916-1 Sequence 1. Appli 34 53 3.1 1416 2 US-08-399-889-1 Sequence 1. Appli 35 53 3.1 1416 2 US-08-399-889-1 Sequence 1. Appli 35 53 3.1 1416 3 US-08-157-364-1 Sequence 1. Appli 36 51.8 3.0 2543 1 US-08-55-669-11 Sequence 1. Appli 39 51.8 3.0 2543 1 US-08-55-669-11 Sequence 11. Appli 39 51.2 3.0 38584 4 US-09-073-663-11 Sequence 11. Appli 39 51.2 3.0 4041 US-09-073-663-11 Sequence 11. Appli 40 50.6 3.0 4031 1 US-09-157-7028-50 Sequence 15. Appli 41 50.6 3.0 4031 1 US-09-159-784-1 Sequence 16. Appli 41 50.6 3.0 4031 1 US-09-147-155-153 Sequence 15. Appli 42 50.2 2.9 9827 4 US-09-247-155-153 Sequence 15. Appli 43 49.8 2.9 1347 4 US-09-247-155-153 Sequence 15. Appli 44 49.2 2.9 1347 4 US-09-247-155-153 Sequence 15. Appli 45 48.8 2.9 1508 4 US-09-247-155-153 Sequence 15. Appli 45 48.8 2.9 1508 4 US-09-29-348-19 Sequence 19. Appli 45 48.8 2.9 1508 4 US-09-29-348-19 Sequence 19. Appli 45 48.8 2.9 1508 4 US-09-29-348-19 Sequence 19. Appli 45 48.8 2.9 1508 4 US-09-29-348-19 Sequence 19. Appli 45 48.8 2.9 1508 4 US-09-29-348-19 Sequence 19. Appli 45 48.8 2.9 1508 4 US-09-29-348-19 Sequence 19. Appli 45 48.8 2.9 1508 4 US-09-29-348-19 Sequence 19. Appli 45 48.8 2.9 1508 5 US-09-188-930A Sequence 19. Appli 50 US-09-188-930A Sequence 19. Appli 60 US-09-188-930A Sequence	8 55.8 3.3 1839 5 PCT-US96-01427-1 Sequence 9 55.6 3.2 4359 4 US-09-484-970B-4 Sequence 0 54.2 3.2 392 4 US-09-404-879A-372 Sequence 1 54.2 3.2 1333 4 US-09-277-357-51 Sequence 2 53.2 3.1 324 4 US-09-404-879A-290 Sequence

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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isola
TITLE OF INVENTION: and Methods For Th
FILE REFERENCE: 11000.1011c1
Query Match 40. Best Local Similarity 82. Matches 819; Conservative
                                           NUMBER OF SEQ ID NOS: 348
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 203
LENGTH: 1123
TYPE: DNA
ORGANISM: Rat
ORGANISM: Rat
S-09-188-930-203
                                                                                                                                                                                                                                            Sequence 203, App. Patent No. 615050
                                                                                                                                                                                                                                 GENERAL
                                                                                                                      CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
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           40.7%;
82.8%;
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Score 696.2; DB Pred. No. 3e-195; 0; Mismatches 16
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RESULT 3 US-09-370-838-151 ; Sequence 151, Application ; Patent No. 6444425

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Patent No. 5869330
GENERAL INFORMATION:
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              SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                        COUNTRY:
APPLICATION NUMBER:
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US/08/463,911
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Pred. No. 5.2e-13;
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US-08-463-911-6
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                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09140804 Patent No. 6197930
                                 NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 4517
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                                                                                                                                                                                                        APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
                                                                                                                                                      CURRENT
                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)
INFORMATION FOR SEQ
                                                                                                               EARLIER APPLICATION NUMBER: 60/056,983 EARLIER FILING DATE: 1997-08-26
ORGANISM: Homo sapiens
                   TYPE: DNA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
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REGISTRATION NUMBER: 32,227
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                                                                                                                                                                                                                                                                                                                                                                                                    ACCACATCACAGTCTATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTTGATGTCATGACTGGTAGATTTGGGGGCCCCAGTATCAGGTGTGTATTTCTTCACCT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAAAGG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATCCCAGGGCATCCGGGCCATAATGGGGCCCCCAGGCCGTGATGGCAGAGATGGCACCC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTATGATGGCTCCACTGGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAACCTGGAGAAGGTGCCTATGTATACCGCTCAGCATTCAGTGTGGGGATTGGAGACTT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTACCCGGG----GATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACCGGAGTACCCGGGGCTGAAGGTCCCCGAGGCTTTCCGGGAATCCAAGGCAGGAAAG
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                                                                                                                                                  APPLICATION NUMBER: US/09/140,804 FILING DATE: 1998-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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ID NO: 6
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50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 204;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5691197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 i.
MEDIUM TYPE: 720 Kb storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
ent No. 5691197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                 ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 CTGGTGAGAAGGGTGAGAAAGGAGATCCAGGTCTTATTGGTCCTAAGGGAGACATCGGTG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GCATCCCAGGGCATCCGGGCCATAATGGGGCCCCAGGCCGTGATGGCAGAGATGGCACCC 210
                                                                                                                                                    COMPUTER: IBM PS/2, Model 5
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                            STREET: 1100 Superior STREET: Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fay, Sharpe, Be
ADDRESSEE: Minnich & McKee
                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTATGATGGCTCCACTGGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCT 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACCTTATGCACAATG 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTTACTATCCCCAACATGCCCATTCGCTTTACCAAGATCTTCTACAATCAGCAAAACC 450
                                                                                                                                                                                                                                                                                        TRY: U.S.A.
44114-2518
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                                                                                                                                                                                                                                                                                                                                   Ohio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kangas, Maarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elomaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tryggvason, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                    Fay, Sharpe, Beall, Fagan
    NUMBER:
                                                                                      435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 5691197el Macrophage Receptor with a Collagenous Domain and the Polypeptide Chain Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An Insolated DNA Sequence For
                                                                                                                                                                                     2, Model 35 SX
DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such a Sequence
                                                                                                                          US/08/392,367B
                                                                                                                                                                                                                                                                                                                                                                                               Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Patent No. 6063901
; TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08893467A Patent No. 6063901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        COUNTRY:
2IP: 44114-2518
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch
MEDIUM TYPE: 720 Kb storable
MEDIUM TYPE: 1BM PS/2, Model 35 SX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1868 base pairs
TYPE: Nucleic acid
STRANDENNESS: Single
                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J
                                                                                                   OPERATING SYSTEM: DOS 5.0
SOFTWARE: WOR'D PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/E
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 GTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCCACCGGGCCCTC 260
                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                 CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 Superior Avenue STREET: Suite 700
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fay, Sharpe, Beall, ADDRESSEE: Minnich & McKee
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  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCCAAAGGAGAAGGGCTACCCGGGGATTCCACCAGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCGTGATGGAACCCCAGGTGTCCAAGGACCCCAGGGCCCACCAGGCAGCAAGGGAGAGG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCGAGGAGAGGAGGCAGCAAAGGTGACATAGGTCTCACTGGCCCCAAGGGGGAACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGAGCGGGGGGCAGCATG 380
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                                                                                                                                                                                                                                                                                                                Ohio
                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (216) 241-1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kangas, Maarit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tryggvason,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No. 5691197 relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elomaa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linear
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No. 5691197 relevant
Richard J.
MBER: 24,175
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58.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such a Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 6063901el Macrophage Receptor
                                                                                                       US/08/893,467A
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                                                                                                                                                                                                                                3.50 inch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72.8; DB 1;
Pred. No. 2.2e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08463911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
                               TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: :
                                                               ATTORNEY/AGENT INFORMATION:
NAME: Granahan; Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
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                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Scherer, Philip
APPLICANT: Lodish, Harvey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 CCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGGAGCGGGGGCAGCATG 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1868 base pairs TYPE: Nucleic acid STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: ~02173
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                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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1276 base pairs
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16) 241-1666
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Harvey F.
A NOVEL SERUM PROTEIN PRODUCED
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                                                                                                  WHI95-05
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                                                                                                                                                                                                                                                                                                                                                                                                       Smith & Reynolds,
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; LOCATION:
US-08-463-911-1
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-794-795-5
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Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Elshou
            SOFTWARE: FASTLERO for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,795
                                                                                                                                                                                                                                                                               APPLICANT: Adamou, John
APPLICANT: Gross, Mitchell
APPLICANT: Lysko, Paul
TITLE OF INVENTION: Human Macro Scavenger Rec
TITLE OF INVENTION: eptor
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
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                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 ATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 GCATCCCAGGACATCCTGGCCACAATGGCACACCAGGCCGTGATGGCAGAGATGGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 GCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 ACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTTGAGACCAACATTGGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 ACAAAGGTGACCTGGGGCCTCGAGGGGGAGCGGGGGCAGCATGGCCCCAAAGGAGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                        CITY: King of Prussia
                                                                                                                                                                                                             STREET:
                                                                                                                                                           COUNTRY:
 FILING DATE:
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                                                                                                                                                                                                               709 Swedeland
                                                                                                                                                           USA
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                                                                                     IBM Compatible
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04-FEB-1997
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                                                     2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671
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Length 1560 Indels

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US-09-249-200-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: 04-FEB-1997
                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LYSKO, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GROSS, MITCHELL APPLICANT: LYSKO, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: ATGS0
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              726 AACTGGAACTAAGGGAGAGAAGGAGACCTGGGTCTCCCA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 GCATGGCCCCAAAGGAGAGAGGGCTACCCGGGGATTCCA 415
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                                                                                                                                                                                                                                                                                 STREET: P.U. BUA CITY: Valley Forge
                                                                         CLASSIFICATION:
                                                                                        APPLICATION NUMBER: US/09/249,200 FILING DATE: 12-FEB-1999
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-4026
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGACCCCAAGGAGAAGGGCAAAGGCGATGGGGGTCTCATTGGCCCCAAAAGGGGGA
                                                                                                                                                                                                                                          19482
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                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSHOURBAGY, NABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                Ratner & Prestia
O. Box 980
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56.8%;
                                                                                                                                                                                                                                                                                                                                                                                         HUMAN MARCO SCAVENGER RECEPTOR
                                08/794,795
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60/017,699
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Pred. No. 5.2e-10;
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US-08-794-795-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1,
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Best Local Similarity 56.8%;
         APPLICATION NUMBER: US/08/
FILING DATE: 04-FEB-1997
CLASSIFICATION: 43-5
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ATG500
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: HAD, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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MOLECULE TYPE:
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TELEFAX: bic
Tex: 846169
                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 19406
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                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                         STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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Lysko, Paul
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                                                                                                                                                                                                                 IBM Compatible
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                                                                                                                                          US/08/794,795
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Pred. No. 5.
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US-09-249-200-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ELSHOURBAGY, NAB
APPLICANT: ADAMOU, JOHN
APPLICANT: GROSS, MITCHELL
APPLICANT: LYSKO, PAUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ATTELECOMMUNICATION INFORMATION: 10-270-5219
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                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 12-FEB-199
                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: 04-FEB-1997
                  TELECOMMUNICATION INFORMATION:
                                                                                 FILING DATE: 23-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641
                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                              NAME: Prestia, Paul F
REGISTRATION NUMBER: 23
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                             COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                    APPLICATION NUMBER: 60/017,699 FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGA 315
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Similarity 56.4%;
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                                                                                                                                                                                                                                                           SYSTEM: DOS
FastSEQ for Windows Version 2.0
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610-407-0700
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                                                                                                                                                                                                            12-FEB-1999
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                                                                                                                                                         08/794,795
                                               23,031
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                                  ATG-50009-1
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Pred. No. 1.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Degenerate nucleotide sequence encoding the zsig39; OTHER INFORMATION: polypeptide of SEQ ID NO:2. US-09-140-804-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-140-804-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 124; Conserv
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sheppard, Paul O.

APPLICANT: Humes, Jacqueline M.

TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

FILE REFERENCE: 97-49

CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT APPLICATION NUMBER: 08-26

EARLIER FILING DATE: 1998-08-26

EARLIER FILING DATE: 1997-08-26

NUMBER: OF SEO, ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Appli
Patent No. 6197930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 TATGGGACGAGATGGAACAACAGGCCCCTCGGGACCCCAAGGCCCACCGGGAGTCAAGGG 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 TAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376
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404 CCGGGGATTCCACCAGAACTTCAGATTGCATTCATGGCTTCTCTGGCAACCCACTTCAGC
                                                                                                                       172
                                                                                                                                                             284 AACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAGGTGAGAAGGGCGACAAA 343
                                                                                                                                                                                                     112 CCNGGNCAYCAYGAWSNCARGGNYTNCCNGGNWGNGAYGGNMGNGAYGGNMGNGAYGGN 171
                                                                                                                                                                                                                                             224 CGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCATTCCAGGAAACCATGGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701 AACTGGAACTAAGGGAGAGAAAGGAGACCTGGGTCTCCCA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1703 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 610-
TELEX: 846169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGGGCA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGACCCCAAGGAGAAGGGCAAAGGCCAATGGGGGTCTCATTGGCCCAAAAGGGGA 700
                                                                             GCNCCNGGNGCNCCNGGNGARAARGGNGARGGNGGNMGNCCNGGNYTNCCNGGNCCNMGN 231
                                          GGNGAYCCNGGNCCNMGNGGNGARGCNGGNCCNGCNGGNCCNACNGGNCCNGCNGGNGAR
                                                                                                                                                                                                                                                                                     164;
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                                                                                                                                                                                                                                                                                   3.7%; Score 63.6; DB 4;
28.2%; Pred. No. 6.7e-09;
7ative 72; Mismatches 343
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Pred. No. 1.6e-09;
0; Mismatches 96;
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: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 19
: LENGTH: 750
: TYPE: DNA
: ORGANISM: RAt
US-09-188-930-19
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US-09-188-930-19
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Best Local Similarity 56.0%;
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
    567
                  387 AAGGAGAGAAGGGCTACCCGGGGATTCCA 415
                                                                                                                                                                                       267 TTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAG 326
                                                                                                                                                                                                                                 387 ACGGCCAGGACGGAGACCGAGGGGACAGTGGAGAAGGAGGTCCACCTGGCAGGACAGGCA 446
                                                                                                                                                                                                                                                                        207 ATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGCCACCGGGCCCTCCTGGCA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 TGYWSNGTNCCNCCNWGNWSNGCNTTYWSNGCNAARWGNWSNGARWSNMGNGTNCCNCCN
                                                                        GACCCAAGGGGGTCAGTGGTACCCCCGGGAAACATGGTATACCGGGCAAGAAGGGACCTA
                                                                                                            GTGAGAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGAGCGGGGGGCAGCATGGCCCCA 386
                                                                                                                                                      ACCGAGGAAAACAAGGACCAAAAGGCAAAAGCTGGGGCCATTGGGAGAGCGGGTCCTCGAG
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AGGGCAAGAAAGGGGAACCTGGGCTCCCA 595
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                                                                                                                                                                                                                                                                                                                  Score 61.8; DB 3; Length 750; Pred. No. 2.3e-08; 0; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                0;
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Search completed: January 15, Job time: 100 secs
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US-09-188-930-217
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 217
LENGTH: 1107
TYPE: DNA
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Best Local Similarity
Matches 117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
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                                                                                                                                                                                                                                                                                         379 ACGGCCAGGACGGAGACCGAGGGGACAGTGGAGAAGAAGGTCCACCTGGCAGGACAGGCA 438
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                                                                                                                                                                                                                                                    267 TTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGTCATGAAGGAGCCAAAG 326
                                                                                                                                          GACCCAAGGGGGTCAGTGGTACCCCCGGGAAACATGGTATACCGGGCAAGAAGGGACCTA 558
                                                                                                                                                                  GTGAGAAGGGCGACAAAGGTGACCTGGGGGCCTCGAGGGGGGAGCGGGGGAGCATGGCCCCA 386
                                                                     AGGGCAAGAAAGGGGAACCTGGGCTCCCA
                                                                                                          AAGGAGAGAAGGGCTACCCGGGGATTCCA 415
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               2003, 19:33:31
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Pred. No. 2.9e-08;
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Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
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Maximum DB seq length: 2000000000
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1367
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1: /SIDS2/acadata /
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compug
//SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
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22 22	21 22	23	22	21	21	21	DB
AAE06589	AAB29582 AAM99925	AAU84371 AAU84370	AAB88447	AAB18909	AAB29580	AAB15548	ID
Human polypeptide Human protein havi	Mouse zacrp2 prote Human polypeptide	Novel human secret	Human membrane or	A novel polypeptid	Human adipocyte co	Human immune syste	Description

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52	0910	AAY91666	52	AAW09108	ABB80583		43	ω	AAU19557	148	30)37	AAB37344	AAB50371	AAE09444	\sim	0	4	944	7217	597	σ	224	04	610	43	216	7210	AAB55964	59	602	AAY75969	M4007	AAY11485	
Mouse OBG3 protein			Human secreted pro	Human adipocyte co	Human sbg1033026C1	₽	A polypeptide desi	Human adipocyte co	Human diagnostic a	Human ovarian anti	Rat protein isolat	•	Murine ACRP30RlM.	Human ZACRP7. Hom	Human SBhACRP30a p	Human genset metab	Novel human protei	novel polyp	D)	rotei	Skin cell protein,	Rat skin cell prot	۳.	Skin cell protein,	Rat skin cell secr		protein	at protei	Skin cell protein,	Skin cell protein,	skin cell pro	Rat skin cell prot	n polypeptid	Human 5' EST secre	

ALIGNMENTS

RRESULT 1
AAB1548
IID AAB1548
XX AAB1548
AC AAB1
XX AAB2
DT 28-F
DT 28 Human immune system molecule from Incyte clone 1890540. 28-FEB-2001 AAB15548; AAB15548 standard; Protein; (first entry) 246 A

Anti-inflammatory; keratolytic; anti-HIV. anti-allergic; antianaemic; antiarteriosclerotic; antiasthmatic; antiabetic; nephrotropic; cancer; antigout; dermatological; antithyroid; virucide; hepatotropic; antibody; immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial; gene therapy; diagnostic; immunological disorder; viral infection; bacterial infection; fungal infection; parasitic infection; immunogen

Homo sapiens.

WO200060080-A2

12-OCT-2000.

04-APR-2000; 2000WO-US09072

05-APR-1999; 05-MAY-1999; 99US-0127852. 99US-0132647.

(INCY-) INCYTE PHARM INC.

Yue H, Lal P, Tang YT, Baughn MR, Azimzai Y, Lu DAM;

WPI; 2000-665005/64.

N-PSDB; AAA95787

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RESULT 2
AAB29580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC may be used to treat or prevent disorders associated with decreased CC expression or activity of IMOL, such as immunological disorders associated with decreased CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease).

CC haematopoletic cancer, infections caused by virus (e.g. adenovirus, CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus, CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g. CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also CC useful as immunogens for the development of antibodies that CC specifically recognizes these peptides. The polynucleotides may be used CC to detect and quantify gene expression in biopsied tissues in which CC expression of IMOL may be correlated with the disease, as targets in a CC compounds in drug screening techniques. Antibodies which specifically CC carrier and affected individuals, and for screening libraries of CC compounds in drug screening techniques. Antibodies which specifically CC bind to IMOL may be used for the diagnosis of disorders characterized CC with IMOL or agonists, antagonists, or inhibitors of IMOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 85; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human immune system molecules 1-15 and polynucleotides encoding them useful for diagnosing, treating or preventing e.g. immunological disorders, infections, cell proliferative disorders, microbial
Human zacrp3; adipocyte complement related
                                       Human adipocyte complement related protein homologue zacrp3, SEQ ID
                                                                              19-FEB-2001
                                                                                                                                                          AAB29580 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AAA95775-A95789), and compositions comprising them are useful for the diagnosis, treatment or prevention of immunological disorders, infections and cell proliferative disorders, including cancer. The IMOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                      LLFETK 246
                                                                                                                                                                                                                                                                                               LLFETK 246
                                                                                                                                                                                                                                                                                                                                                                             YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGIPGNHGNNGANGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents a human immune system molecule (IMOL) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGIPGNHGNNGNNGATCHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
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                                                                              (first entry)
                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1367;
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protein homologue
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MASLATHESNONSGIIESSVETNIGNEFDVMTGREGAPVSGVYEFTESMMKHEDVEEVYV

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PPG I PGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPG I PPELQIAF PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120

MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV

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61 61 ۲ Qy

1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG

60 60

Query Match Best Local Similarity Matches 246;

100.0%;

Score 1367; DB 2 Pred. No. 2e-124; Mismatches

21; 0;

Indels Length 246;

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Gaps

0;

Conservative

0;

Sequence

246 AA;

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The invention relates to the human zacrp3 protein (AAB29580) and to nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homogue of adipocyte complement related protein (ACRP30) and contains a collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and C-terminal Clq domain comprising 10 beta-strands. The zacrp3 gene is located on chromosome 5pl2. The invention also relates to zacrp3 fragments, fusion proteins containing zacrp3 polypeptides, zacrp3-specific antibodies, expression constructs and host cells comprising zacrp3 nucleic acids, and methods of recombinant production carcrp3. Human zacrp3, and its agonists and antagonists may be used in the study and modulation of cellular metabolism and energy balance in
                                                                                                                                 anorexia, and conditions associated with these disorders. Due to its Clq like domain, zacrp3 and zacrp3-containing fusion proteins may be useful as antimicrobial agents, promoting lysis or phagocytosis of infectious organisms such as bacteria or viruses. Zacrp3, its fragments, fusion proteins, antibodies and activity modulators may also be used to inhibit collagen-induced platelet aggregation, adhesion, or activation, and may therefore have potential for promoting blood flow within the vasculature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel zacrp3 polypeptides used to treat or prevent bacterial infections, for wound healing, improving blood flow, and to a energy efficiency in mammals -
                                                                                        of a mammal e.g., to treat injury to the vasculature or other collagenous tissue. Human zacrp3 and its antibodies may additionally be used to study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 109-110; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACRP30; Clq domain; collagen-like domain; energy balance modulat: cellular metabolism; metabolic disorder; obesity; anorexia; antimicrobial agent; infection; platelet aggregation inhibition; adhesion; activation; vascular injury; antibacterial; antiviral.
                                                                   dimerisation and oligomerisation. The present sequence represents human
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                                                                                                                                                                                                                                                                                                    mammals, and may therefore be used to treat disorders such as obesity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZYMO ) ZYMOGENETICS INC.
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23-MAR-1999;
24-MAR-1999;
31-MAR-1999;
05-APR-1999;
21-APR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122; PRO189; PRO1890; PRO1887; PRO1785; PRO4357; PRO4357; PRO4405; PRO450; PRO4354; PRO44354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6197804424; PRO4422; PRO4439; PRO4499; tumour; obesity; diabetes; insullnemia; kidney disorder; Bergers disease; nephropathy; Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               Crohns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB18909 standard; Protein; 246
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                                                           2000WO-US05601.
               99US-0125778.
99US-0125826.
99US-0127035.
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CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1889, PRO1887, PRO4785, PRO4353, PRO4435, PRO4435, PRO4435, PRO4356, PRO4356, PRO4350, PRO4350, PRO4350, PRO4424, PRO4409, PRO4409, PRO5737, PRO44425, PRO5900,
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4409, PRO51889 polypeptide is
CC useful for diagnosing tumour in amammal. The polypeptides, their
CC appoints and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC expression or activity of the polypeptide. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells
CC and are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing.
                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 APR 1999
27 APR 1999
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25 MAY 1999
20 JUL 1999
20 JUL 1999
03 AUG-1999
09 DEC 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use \,\cdot\,
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers L,
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 2;
100.0%; Score 1367; DB 21; ilarity 100.0%; Pred. No. 2e-124; Conservative 0; Mismatches 0;
                                                                                                                                                       246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eaton DL, (Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9905-0131272
9905-0131291.
9905-0132271.
9905-0132379.
9905-013283.
9905-0135750.
9905-0146791.
9905-0146790.
9905-0170262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard A,
, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godowski PJ,
2hang Z;
                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan
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Matches 246;
                               181
                                          121
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241 LLFETK 246
                                                             MASLATHFSNONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV 180
                   LLFETK 246
                                                                                                          Indels
                                                                                                          0;
                                                                                                         Gaps
                     240
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Local Similarity

AAB88447 standard; Protein;

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QY
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                                                                                                                                     Matches
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11-JAN-2000;
                                                                                                                                                                                                                                                  (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAB88317 - AAF82235 which are used to isolate aAAF93917 - AAF94295 and AAAF62232 - AAF62235 which are used to isolate cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                          arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1067182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human membrane or secretory protein clone PSEC0232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB88447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2001
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 61
                            61
                                                                                                                                                      Local
                PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF
                                                                                   MLWRQLIXWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to nucleic acid sequences AAF93744 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-093989/11
                                                                  MEWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secretory protein; membrane protein; vaccine; gene therapy;
toid arthritis; diabetes.
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF93874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID 262; 609pp + CD ROM; English.
                                                                                                                                                                                                        246
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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2000JP-0183766
                                                                                                                                                                                                        AA;
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                                                                                                                                                    100.0%;
                                                                                                                                     0,:
                                                                                                                                  Score 1367;
Pred. No. 2e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF62235 which are used to isolate the
                                                                                                                                                      2e-124;
                                                                                                                                                                    DB 22;
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                                                                                                                                    Indels
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                                                                                                                                  Gaps
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RESULT 5
AAU84371
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                                                                      amellorating various diseases such as inflammatory disorders (e.g. asthma), neurological disorders (e.g. dementia), haematopoietic disorders, skeletal developmental disorders, growth abnormalities, neurodegenerative disorders (e.g. Huntington's disease), nervous system neurodegenerative disorders (e.g. Huntington's disease), nervous system disorders, autoimmune disorders (e.g. rheumatoid arthritis), peripheral myelinopathies, viral and bacterial infections, alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK )
(SMIK )
(GLAX )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disorder; neurological disorder; haematopoietic disorder; skeletal developmental disorder; growth abnormality; autoimmune disorder; neurodegenerative disorder; neurous system disorder; bacterial infection; peripheral myelinopathy; viral infection; cancer; obesity; diabetes; hypotension; sexual development disorder; blood disorder
                                                                                                                                                                                or membrane-associated proteins and the genes encoding them. The sequences of the invention are useful for treating, preventing and
                                                                                                                                                                                                                                                                                          encoding the polypeptides, for preventing, treating cancers, mental or sexual developmental disorders,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-188468/24
                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                        Novel secreted and membrane-associated polypeptides encoding the polypeptides, for preventing, treating
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK35591.
                                                                                                                                                                                                                                                                                                                                                                                                                   Agarwal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUL-2000;
21-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human secreted or membrane-associated protein #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU84371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted protein; membrane-associated protein; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SMITHKLINE BEECHAM CORP
SMITHKLINE BEECHAM PLC.
GLAXO GROUP LTD.
                                                                                                                                                                                                                                           Page 131-132; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   Xiang
                                                                                                                                                                                                                                                                                                                                                                                                                     Cogswell JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-218033P
2000US-226517P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US21985
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                                                                                                                                                                                                                relates to the isolation of novel human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                     Lai Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                     Martensen
                                                                                                                                                                                                                                                                                                                                                                                                                     SA,
                                                                                                                                                                                                                                                                                                                                                                                                                     Rizvi
                                                                                                                                                                                                                                                                                          and malignant tumours
                                                                                                                                                                                                                                                                                                        and polynucleotides and ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                     SK,
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                                                                                                                                                                                                                                                                                                                                                                                                                     JC;
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or sexual development disorders, and dysfunctions of the blood cascad system including those leading to stroke. AAU84362-AAU84389 represent the novel human secreted or membrane-associated proteins of the hypotension, obesity, bulimia, anorexia, manic depression, delirium, mental retardation, Tourette's syndrome, schizophrenia, growth, ment

yndrome, schizophrenia, growth, mental and dysfunctions of the blood cascade

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                              encoding cancers,
                                                                                                                                                                                                                                                                                                            Human; secreted protein; membrane-associated protein; hypertension; inflammatory disorder; neurological disorder; haematopoietic disorder; skeletal developmental disorder; growth abnormality; autoimmune disorder; neurodegenerative disorder; nervous system disorder; bacterial infection; peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                          WO200204600-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU84370 standard;
                              Novel secreted and membrane-associated polypeptides and polynucleotides encoding the polypeptides, for preventing, treating and ameliorating cancers, mental or sexual developmental disorders, and malignant tumour.
                                                                                                                                                                                                                 12-JUL-2001; 2001WO-US21985
                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted or membrane-associated protein #9.
                                                                                                                  Agarwal P,
                                                                                                                                                                                           12-JUL-2000;
                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                   hypotension; sexual development disorder; blood disorder
                                                                                                                                        (GLAX)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
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                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MASLATHFSNONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246;
                                                                                                                                      SMITHKLINE BEECHAM
SMITHKLINE BEECHAM
GLAXO GROUP LTD.
                                                                         ABK35590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 AA;
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                                                                                                                  Cogswell JP,
                                                                                                                                                                                 2000US-226517P
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                                                                                                                                                                                           2000US-218033P
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
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                                                                                                         Ö
                                                                                                                  Lai Y,
                                                                                                                                                   PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                   Martensen
                                                                                                                   SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
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                                                                                                                   Rizvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                malignant tumours
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                                                                                                                   Strum
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Claim 1;

Page 130-131; 151pp; English

19-APR-2000; 2000WO-US10454.

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RESULT 7
AAB29582
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Best Local :
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                                                                                                                Mouse zacrp2; adipocyte complement related protein homologue; ACRP30; Clq domain; collagen-like domain; energy balance modulat: cellular metabolism; metabolic disorder; obesity; anorexia; antimicrobial agent; infection; platelet aggregation inhibition; adhesion; activation; vascular injury; antibacterial; antiviral; human zacrp3 homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel human s or membrane-associated proteins and the genes encoding them. Th sequences of the invention are useful for treating, preventing ameliorating various diseases such as inflammatory disorders (e
                                                                                                                                                                                                                                                                                          AAB29582
                                                                                                                                                                                                                                                                                                                        AAB29582 standard; Protein; 246 AA.
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                                                         WO200063377-A1
                                                                                        Mus musculus
                                                                                                                                                                                                                             Mouse zacrp2
                                                                                                                                                                                                                                                           19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                                                                                                               HGDHQRFSTFAGFLLFETK 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTF
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246; Conserv
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                                                                                                                                                                                                                             protein,
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77.1%;
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Pred. No. 9.3e-120;
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                                                                                                                                                                                 modulation;
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RESULT 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a mammal e.g., to treat injury to the vasculature or other collagenous tissue. Human zacrp3 and its antibodies may additionally be used to study dimerisation and oligomerisation. The present sequence represents mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel zacrp3 polypeptides used to treat or prevent bacterial or viral infections, for wound healing, improving blood flow, and to analyze energy efficiency in mammals -
            AAM99925;
                                      AAM99925 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zacrp2, a homologue of human zacrp3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 117-118; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                                           MASLATHFSNONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV 180
                                                                                                                                                                                                                                                                     PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                                                                                                                                            LLFETK 246
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                                                                                                                                                                                                                                                                                                                                                                                      236;
                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                       225 AA
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Pred. No. 5.5e-119;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 246;
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PD XX PF XX
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14-JUL-2000

0000S-0220963 0000S-0220964

2000US-0216880. 2000US-0217487. 2000US-0217496.

2000US-0214886 2000US-0215135

2000US-0209467 2000US-0205515 2000US-0198123 2000US-0190076 2000US-0189874 2000US-0186350 2000US-0184664 2000US-0180628

2000US-0216647

19-MAY-2000; L8-APR-2000; L6-MAR-2000;

01-SEP-2000; 01-SEP-2000; 01-SEP-2000;

01-SEP-2000;

30-AUG

18 - AUG 14 - AUG 14 - AUG 14 - AUG

2000US-0225267 2000US-0225268

2000US-0225214 2000US-0225266 2000US-0225213 2000US-0224518 2000US-0218290

08-SEP-2000; 08-SEP-2000;

08-SEP-2000; 08-SEP-2000;

> 2000US-0232080 2000US-0231413. 2000US-0231414.

2000US-0232081.

2000US-0231968. 2000US-0232397. 2000US-0232398.

08-SEP-2000; 08-SEP-2000; 06-SEP-2000; 06-SEP-2000; 05-SEP-2000; 05-SEP-2000;

> 2000US-0231242 2000US-0230437

2000US-0230438 2000US-0229513 2000US-0229509 2000US-0229345 2000US-0229344 2000US-0229343 2000US-0229287 2000US-0228924 2000US-0227009 2000US-0227182 2000US-0226868 2000US-0226681 2000US-0226279 2000US-0225759 2000US-0225758 2000US-0225757 2000US-0225447 2000US-0225270

08-SEP-2000;

2000US-0231244

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                       Human polypeptide SEQ ID NO
                                                                                                                                                                                                             07-JAN-2002 (first entry)
                  Homo sapiens.
                                                        neurological disease; infection; human; secreted protein.
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17-JAN-2001;

2001WO-US01356

2000US-0232400. 2000US-0232401. 2000US-0233063.

2000US-0233065

21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 26-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000

2000US-0235834 2000US-0235484 2000US-0234998 2000US-0234997

2000US-0235836

2000US-0236370 2000US-0236369 2000US-0236368 2000US-0236367 2000US-0236327

2000us-0237038

2000US-0237039

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Best Local Sim
Matches 218;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directl from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and the encoded proteins (AAM99915-AAM99934) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, liver, autoimmune haemolytic anemia, autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids and polypeptides, useful for treating, preventing ameliorating human disorders and diseases \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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             Human polypeptide SEQ ID NO 6791.
                                                                     AAM41860;
                                                                                                AAM41860 standard; Protein; 202 AA
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                                         22-OCT-2001 (first entry)
                                                                                                                                                                       187
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                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                         invention relates to novel human polynucleotides (AAI99513-AAI99538) the encoded proteins (AAM99915-AAM99934) which are useful for
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                                                                                                                                                                     AVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGFLLFETK 246
                                                                                                                                                                                                                          11; SEQ ID NO 41; 465pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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2000US-0251856
2000US-0251868
2000US-0251869
2000US-0251989
2000US-0251990
2000US-0251990
2000US-0251997
2000US-0254097
2001US-0259678
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Pred. No. 4.9e-109;
1; Mismatches 0;
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2000US-0246532. 2000US-0246609. 2000US-0246610.

2000US-0246528 2000US-0246526 2000US-0246525

2000US-0246527

2000US-0246524 2000US-0246478 2000US-0246476 2000US-0246474 0000S-0244617

17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 01-DEC-2000 01-DEC-2000 05-DEC-2000 05-DEC-2000

2000US-0249299. 2000US-0249300. 2000US-0250160. 2000US-0250391.

2000US-0249264. 2000US-0249265. 2000US-0249297.

17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249217. 2000US-0249218. 2000US-0249244.

2000US-0249245

17-

17-NOV-2000; 17-NOV-2000;

NOV-2000;

2000US-0249214 2000US-0249215

2000US-0249213 2000US-0249212

2000US-0249216

17-NOV-2000; 17-NOV-2000;

2000US-0249208. 2000US-0249209. 2000US-0249210. 2000US-0249211.

2000US-0249207 2000US-0246613 2000US-0246611

NOV-2000;

20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

2000US-0246475

2000US-0241808

2000US-0241785 2000US-0240960 2000US-0239937

2000US-0241809 2000US-0241826

13-OCT-2000

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                          system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 6791; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                         specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
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                                                                      2001-442253/47.
DB; AAI61016.
               FTFSMMKHEDVEEVYYYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN 224
                                                                                                                                                                                     TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPE-----
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FTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN
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170; Conser
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                                                                                                                                                                                                                                                                                                                                                           The sequence
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                                                                                                                                                                                                                                                                                                                                                                                            for receptor activity, arthritis and
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                    202 AA;
                                                                                                                                                                                                                            Conservative
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2000US-0620312.
2000US-0653450.
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2000US-0693036.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                           data
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                                                                                                                                                                                                                                            64.7%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for treating disorders system injuries -
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                                                                                                                                                                                                                                          Score 884; DB 22;
Pred. No. 1.2e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              u C, Xue
Drmanac R
                                                                                                                                                                                                                          Mismatches
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Xue AJ,
? RT;
                                                                                                                                                                                                                                                                                                                                                                                          and therapy, drug screening, inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                       not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                             202;
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                                                                                                                                                                                                                      Gaps
180
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fertility), to modulate chemotactic and chemokinetic activity, modulate haemostatic and thrombolytic activity, to modulate re

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receptor growth.

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В
                                                                                                               CC HP10781. The polynuclectide and polypeptide of the invention (CC may be used in the prevention, diagnosis and treatment of diseases (CC associated with inappropriate polypeptide expression. The polynucleotides (CC into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA (CC polynucleotides and its complementary sequences may also be used as DNA (CC polypeptides may also be used as antigens in the production of antibodies (CC and in assays to identify modulators of polypeptide expression and (CC activity. The polypeptides and nucleic acids may be used as nutritional (CC supplements, to modulate cytokine and cell proliferation activity, to (CC modulate immune stimulation or suppression (e.g. for the treatment of medulate incoming and insulin-dependent diabetes), to modulate (CC contents), to modulate incoming this polypeptide is tissue growth activity (e.g. for the contents), to modulate activin and insulin-dependent diabetes and Alzheimer's (contents), to modulate activin and inhibit activity (e.g. for controlling (e.g. for the controlling controlling the polypeptides activin and inhibit activity (e.g. for controlling controlling controlling the polypeptides activing and inhibit activity (e.g. for controlling controlling controlling the polypeptides activing and inhibit activity (e.g. for controlling con
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03-FEB-2000;
03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer^\prime s and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell proliferation; immunomodulatory; aurumunc community insulin-dependent diabetes; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; cytostation are in the community of the community of the community in the community of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE06589
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haemostatic; thrombolytic; tumour growth inhibitor; anabolic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is human protein with hydrophobic domain,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000JP-0000585.
; 2000JP-0000588.
; 2000JP-0002299.
; 2000JP-0026862.
; 2000JP-0058367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563pp; English.
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AAV11485
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COC Human
KW Human
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AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY11374 to AAY11531, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, hemmatopoicsis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic activity.
                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids encoding human secreta
cDNA libraries prepared from substantia
and fetal brain tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 5' EST secreted protein SEQ ID No 307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                  Claim 34; Page 402-403; 434pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duclert A, Dumas Milne Edwards J, Lacroix B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY11485 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9906551-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-IB01235
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                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted
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                                                                                                                                                                                                                                                                                                                                                                                                       proteins obtained from ra, cerebellum, surrena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                      peptide
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                                                                                                                                                             09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                         Wang
                                                                                                     Tang
                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products
                                                                                                                                                                                                                         21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                             26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                                                                                                                                                            WO200153312-A1
                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                        peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM40074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM40074 standard; Protein; 126 AA
                                                                                                                                                    29-NOV-2000;
                                                                                                                             (HYSE-)
                                                                                                                                                                                                                                                                                                                                                          leukaemia
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                                                       2001-442253/47.
                                                                              ος, τη,
                                                                                                                                                                                                                                                                                                                                   sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124;
                                                                                                                                                                                                                                                                                                                                                                                                                   nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                            HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                            Liu C,
Wang z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA;
                                                                                                                                                   2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                                                                                                                                                                 2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                       2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                        Asundi V, (
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3219.
                                                                                                                                                                                                                                                                                                                                                                                                        system;
                                                                               Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.78;
                                                                                                                                                                                                                                                                                                                                                                                                      neuropathy;
                                                                                        Chen R,
Xu C,
                                                                               æ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 721; DB 20;
; Pred. No. 4.2e-62;
0; Mismatches 0;
                                                                              nen R, Ma Y,
Ku C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                        central nervous system;
                                                                                         Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 128;
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                                                                                          Zhang
                                                                                                     Ren F,
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                                                                                                                                                                                                                                                                                                                                                                                                         CNS;
                                                                                                     Wang
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                     Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.N.S
                                                                                                                                                                                                                              WO9955865-A1
                                                                                                                                                                                                                                                           Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY75969 standard; Protein;
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                           WPI; 2000-072177/06
                                                        Strachan L,
                                                                                                                                                                   29-APR-1999;
                                                                                                                                                                                                                                                                                        anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                    Rat skin cell protein, SEQ ID 147.
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification.
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                                                                                      (GENE-) GENESIS RES & DEV CORP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic, unosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLFETK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLMHNGNTVFSMYSYENKGKSDTSSNHAVLKLAKGDEVWLRNGNGALHGDHQRFSTFAGF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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                                                         Sleeman
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                                                                                                                     98US-0069726.
98US-0188930.
                                                                                                                                                                   99WO-NZ00051.
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100.0%;
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                                                         Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 663;
Pred. No.
                                                                                                                                                                                                                                                                                          neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                         Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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                                                         Kumble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                         A
                                                         Murison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                       cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                         JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Novel polynucleotides useful for

the

treatment of various

conditions

Novel polynucleotides useful for the treatment of various

conditions

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RESULT 14
AAY76025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          рЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukcoytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and AAY76119 are secreted. Sequences AAY75986-V75989, AAY76061-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation
                                                                                                                                                                                                                                                                                                                                               Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell secreted; transmembrane; inflammation; cancer; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 112-113; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel nucleic acid sequences derived from rat
                          WPI; 2000-072177/06
N-PSDB; AAZ61730.
                                                                       Strachan L,
                                                                                                                                   29-APR-1998;
09-NOV-1998;
                                                                                                                                                                               29-APR-1999;
                                                                                                                                                                                                             04-NOV-1999
                                                                                                                                                                                                                                          WO9955865-A1
                                                                                                                                                                                                                                                                         Rattus
                                                                                                                                                                                                                                                                                                    anti-inflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                   angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle diso
                                                                                                                                                                                                                                                                                                                                                                                                              Rat skin cell protein, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY76025 standard; Protein; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              putative transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including wounds and cancer
                                                                                                   (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLRRQLVWWHLLALLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                        Sleeman
                                                                                                                                 98US-0069726
98US-0188930
                                                                                                                                                                               99WO-NZ00051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%;
                                                                        Z
                                                                        Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 582; DB 2
Pred. No. 1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                NO:280
                                                                        JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                        Onrust
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                                                                        Kumble
                                                                                                                                                                                                                                                                                                                      disorder;
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                                                                        Murison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amplifying
                                                                                                                                                                                                                                                                                                                                                                 cell;
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0;

including wounds and cancer -

235pp; English.

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RESULT 15
AAB55908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences AAY75942-Y76123 represent polypeptides encoded types. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences AAY75942-Y76123 represent polypeptides encoded types. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences AAY75942-Y76123 represent polypeptides encoded types. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences AAY75942-Y75947, AAY760121 AAY760121 -Y760121 -Y760121 -Y760121 -Y760121 -Y760121 -Y760121 -Y760121 -Y760121 -Y760121 -Y76012 -Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
                 New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200069884-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skin cell protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001 (first entry)
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                                                                                                                                                                                         Watson JD,
                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                           15-MAY-2000; 2000WO-NZ00075.
                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPG 60
                                                                                                                  2001-007495/01
DB; AAC99566, AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLRRQLVWWHLLALLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                          99US-0312283.
                                                                                                                     AAC99776
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93.3%;
                                                                                                                                                                                         Onrust R,
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Pred. No. 1e-48;
2; Mismatches
                                                                                                                                                                                         Sleeman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.
                                                                                                                                                                                            Kumble KD,
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Best Local Similarity
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                                                                                                                                          Sequence
                                                                                                                                                                                                 (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                   keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                         The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 147; 352pp; English.
                                                                                                                                                                                oligonucleotides for examining expression patterns.
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MLRRQLVWWHLLALLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPG
                  98;
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                                                                       Conservative
                                                                                      42.6%;
93.3%;
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                                                                                        Score 582; DB 2
Pred. No. 1e-48;
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                                                                                                          Length 105;
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Job time : 81 secs Search completed: January 15, 2003, 19:37:10 В QУ

61

PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKG 105

PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKG 105

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Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB seq
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length: 2000000000
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1 MLWRQLIYWQLLALFFLPFC.
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US-09-336-536-3
US-09-118-408-3
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
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	Sequence 2, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 9, Appli	Sequence 12, Appl		Seguence 66, Appl	Sequence 66, Appl		Sequence 66, Appl	Sequence 6, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 138, App	Sequence 5, Appli	Sequence 4, Appli

ALIGNMENTS

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; SEQ ID NO 147
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-147
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US-09-188-930-280
                                                                                                                                                                       ; Sequence 280, Application US/09188930A ; Patent No. 6150502 ; GENERAL INFORMATION:
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Matches
              APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated
TITLE OF INVENTION: and Methods For Their
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 348 SOFTWARE: FastSEQ for Windows Version 3.0
CURRENT APPLICATION NUMBER: US/09/188,930A
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93.3%;
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 Sequence
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Best Local Similarity
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SEQ ID NO 294:
LENCTH: 294
TYPE: PRT
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NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 280
LENGTH: 105
TYPE: PRT
ORGANISM: Rat
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APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
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                                                                                                                                                                   175 PIKFDKILMNEGGHYNASSGKFVCSVPGIYYFTYDITLANKH-----LAIGLVHNGQ--Y 227
                                                                                                                           191 SMYSYEMK-GKSDTSSNHAVLKLAKGDEVWLRM----GNGALHGDHQRFSTFAGFLLF 243
                                                                                                                                                                                                     134 GIIFSSVETNIGNEFDVMTGREGAPVSGVYFFTFSMM---KHEDVEEVYVYLMHNGNTVF 190
                                                                                                                                                                                                                                            115 GPRGPKGVSGTPGKHGIPGKKGPKGKKGEPGLPGPCSCGSSRAKSAFSVAVTKSYPRERL 174
                                                                                                                                                                                                                                                                                      93
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                                                                                                                                                                                                                                                                                                                                                              60 GPPGIPGNHGNNGNNGATGHEGAKGEKGDKGD------
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93.3%;
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Pred. No. 2.1e-51;
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US-09-530-423-2

Sequence 2, Application US/09530423

Patent No. 6461821

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               APPLICANT: Otsuka Pharmaceutical Co., Ltd.
TITLE OF INVENTION: Smooth muscle growth in
TITLE OF INVENTION: diagnostic method for
TITLE OF INVENTION: therefor
FILE REFERENCE: P98-51
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SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                  169 VY--MKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNG
                                                                                                                                                                                                                                                                                                                        171 KHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRM-GNG---A 226
                                                                                                                                                                                                                                                                                                                                                            109 EAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHIT 168
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nes 81; Conserv
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 IPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGER---GQHGPKGEKGYPGIPPE----- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLQALLFLLILP-SHAEDDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48
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SYSTEM: PC-DOS/MS-DOS
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A NOVEL SERUM PROTEIN PRODUCED
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Harvey F.
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US-09-530-423-2
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CURRENT FILING DATE: 2000-05-01
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                                                                                         TELEFAX: (617) 861-954 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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                                                                                                                                                REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                   TOPOLOGY:
                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                  LENGTH:
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Lodish, Harvey F.
VENTION: A NOVEL SERUM PROTEIN PRODUCED
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protein
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Pred. No. 7.6e-22;
5; Mismatches 78;
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LENGTH: 2
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT FILING DATE: 1998-08-26

EARLIER APPLICATION NUMBER: 60/056,983

EARLIER FILING DATE: 1997-08-26

NUMBER OF SEQ ID NOS: 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS 200
201 VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
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                                   AVLKLAKGDEVWLRM-GNG---ALHGDHQRFSTFAGFLLF 243
                                                                               YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS 200
                                                                                                                                                             TGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNH 142
                                                                                                                                                                                                 RGQHGPKGEKGYPGI-----PPE----LQIAFMASLATHFSNQNSGIIFSSVETNIGNF 147
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                                                                                                                   FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH 207
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                                                                                                                                                                                                                                                                                                                      21.5%; Score 293.5; DB 4; 34.5%; Pred. No. 8.2e-22; mismatches 78;
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Pred. No. 8.2e-22;
"'cmatches 78;
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US-09-336-536-20

Sequence 20, Application Patent No. 6406884 GENERAL INFORMATION:

APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Otsuka Pharmaceutical Co., Ltd.

TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 244
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LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Abdominal fat tissue from myoma uteri-09-530-423-1
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP H9-297569 PRIOR FILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/530,423 CURRENT FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: 1
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nes 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                           Local
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VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
                                       AVLKLAKGDEVWLRM-GNG---ALHGDHQRFSTFAGFLLF 243
                                                                                 YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS 200
                                                                                                                         FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH 207
                                                                                                                                                                  TGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNH 142
                                                                                                                                                                                                          RGQHGPKGEKGYPGI-----PPE----LQIAFMASLATHFSNQNSGIIFSSVETNIGNF 147
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                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                       21.5%; Score 293.5; DB 4
34.5%; Pred. No. 8.2e-22;
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                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                             DB 4;
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; SEQ ID NO 3; LENGTH: 247; TYPE: PRT; ORGANISM: Homo s
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US-09-118-408-3
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US-09-140-804-8
  Query Match
Best Local S
Matches 82
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Best Local Similarity 31.9
Matches 82; Conservative
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NUMBER OF SEQ ID NOS: 47
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09140804 Patent No. 6197930 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09118408A Patent No. 6265544
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                  EARLIER FILING DATE: 1997-07-18 NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/053,154
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/118,408A CURRENT FILING DATE: 1998-07-17
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS FILE REFERENCE: 97-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS FILE REFERENCE: 97-49
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82; Conserv
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                                                                                                                                                                                                                                                                                                                                               Paul O
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NUMBER: 60/056,983
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Score 287; DB 4; 1
Pred. No. 3.8e-21;
0; Mismatches 101;
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6 LIYWQLLALFFLPFCLCQDEYMESPQTGG--LPPDCSKCCHGDYSFRGYQGPPGPPGPPG 63

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US-09-506-855-3
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                                                                                                RESULT 13
US-08-463-911-4
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; ORGANISM: Homo sapien
US-09-506-855-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
                                     Sequence 4, Application US/08463911 Patent No. 5869330 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
APPLICANT: Scherer, Philipp E. APPLICANT: Lodish, Harvey F.
                                                                                                                                                                                                  227 LHGDHQRFSTFAGFLLF 243
                                                                                                                                                                                                                                                                                                  171 KHEDVEEVYYYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRM-GNG---A 226
                                                                                                                                                                                                                                                                                                                                                                               115 E----LQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMM 170
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                                                                                                                                                                                                                                                          169 VY--MKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 VY--MKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNG 226
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                                                                                                                                                                             227 LYADNVNDSTFTGFLLY 243
                                                                                                                                                                                                                                                                                                                                         109 EAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHIT 168
                                                                                                                                                                                                                                                                                                                                                                                                                         49 HPGHNGTPGRDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPQTPGRKGEPG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 IPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGER----GQHGPKGEKGYP------GIPP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 HPGHNGTPGRDGRDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPQTPGRKGEPG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGER---GQHGPKGEKGYP------GIPP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLQALLFLLILP-SHAEDDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 247;
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RESULT 14
US-09-370-838-185
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                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                            Sequence 185, Application US/09370838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                    CURRENT APPLICATION NUMBER: US/09/370,838 CURRENT FILING DATE: 1999-08-09 EARLIER APPLICATION NUMBER: US 09/285,323 EARLIER FILING DATE: 1999-04-02
                                                                                                         TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR US FILE REFERENCE: 210121.475C1
                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 861-95 INFORMATION FOR SEQ ID NO:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                     19 NSKQVSSGGALLRLQRGDEVWLSVNDYNGMV-GIEGSNSVFSGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 GKSDTSSNHAVLKLAKGDEVWLRMG--NGALHGDHQRFSTFAGFLLF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 YNPSTGKFTCEVPGLYYFVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSM------YSYEMK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 GEKGYPGIP-----PELQ-----IAFMASLATHFSNQNSGIIFSSVETNIGNF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 GTSGLPGDPGPRGPPGEPGVEGRYKQKHQSVFTVTRQTTQYPEANALVRFNSVVTNPQGH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 GCYGIPGMPGMPGKDGHDGLQGPKGEPGIPAVPGTQGPKGQKGEPGMPGHRGKNGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GYQGPPGPPGPPGIPGNHGNNGNNGATGH-----EGAKGEKGDKGDLGPRGERGQHGPK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/463,911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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31.3%; pred. No. 7.6e-20;
Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A NOVEL SERUM PROTEIN PRODUCED EXCLUSIVELY IN ADIPOCYTES
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Gaps

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CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-336-536-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 185
LENGTH: 746
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                                                                                                                                                                                                                                                                                                                      Query Match 19.38
Best Local Similarity 32.48
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09336536
Patent No. 6406884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-336-536-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 LYQ 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 623 RTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRENCPVNGTYVFIFHMLKLAVNVPLYVN 682
217 EVWLRMGNG---ALHGDHQRFSTFAGFLLF 243
:||:::| | :: |||:|||::
189 QVWVQVGVGDYIGIYASIKTDSTFSGFLVY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 LFE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 LATHES -- NONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 QVSSPE-RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYP-LPQQMRVAFSAA 622
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                                                                                 134 GVYYFAV----HATVYRASLQFDLVKNGESIASFFQF-FGGWPKPASLSGGAMVRLEPED 188
                                                                                                                     161 GVYFFTFSMMKHEDVEEVYVY--LMHNGNTVFSMYSYEMKG--KSDTSSNHAVLKLAKGD 216
                                                                                                                                                                                    101 HGPKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVS 160
                                                                                                                                                                                                                                        34 GLPPDCSKCCHGDYS-----FRGYQGPP------GPPGPPGIPGNHGNNGNN 74
                                                                                                                                                             74 AGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 GATGHEGAKGEKGDKGDLGPRGERGQ-----HGPKGE----KGYPGIPPELQIAFMAS 123
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                                                                                                                                                                                                                                                                                                                                               19.3%;
                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                                                                                                                                                                        Score 264.5; DB 4; Length 228;
Pred. No. 6.3e-19;
6; Mismatches 79; Indels 27
                                                                                                                                                                                                                                                                                                                          27;
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Search completed: January 15, 2003, 19:41:37 Job time: 37 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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208 AVLKLAKGDEVWLRM-GNG---ALHGDHQRFSTFAGFLLF 243

A;Accession: A;Molecule t A;Residues: A;Cross-refe A;Experiment R;Nakano, Y A;Title: Isc A;Reference A;Accession: A;Mitle: Isc A;Reference A;Accession: A;Molecule t A;Residues: C;Comment: I C;Genetics: C;Comment: I C;Genetics: C;Keywords: F;11-14-Domair F;19-244/pr F;42-107/Reg F;114-241/pc F;95/Modifie F;230/Bindin Query Matc Best Local Matches Qy 53 QQ Qy 98 RQ Qy 98 RQ Qy 98 RQ Qy 98 RQ Qy 148 FI Db 83 TG	30 32 32 33 33 34 35 35 36 37 37 38 39 39 39 39 44 42 42 42 42 42 42 43 44 45 45 45 47 47 47 48 48 48 48 48 48 48 48 48 48 48 48 48
A; Accession: JC4708 A; Accession: JC4708 A; Accident type: mRNA A; Residues: 1-244 < MA A; Residues: 1-244 < MA A; Residues: 1-264 < MA A; Cross-references: D A; Experimental source B; Nakano, Y; Tobe, T J. Biochem. 120, 803- A; Title: Isolation an A; Reference number: J A; Accession: JC4944 A; Molecule type: prote C; Genetics: 19-38 93- C; Comment: This prote C; Genetics: adipose t C; Reywords: adipose t C; 114-241/Domain: conl F; 125/Modified site: C Query Match Best Local Similari Matches 76; Cons Query Match Best Local Similari Best Local Si	30 201 14.7 215 31 197 14.4 17 32 196 14.3 1214 33 195.5 14.3 1744 35 193.5 14.1 296 36 193.5 14.1 296 37 193.5 14.1 301 38 192.5 14.1 301 38 192.5 14.1 921 39 192.5 14.1 921 39 192.5 14.1 921 40 190.5 13.8 13.8 136 41 189 13.8 137 42 189 13.8 137 42 189 13.8 375 43 189 13.8 1464 44 187.5 13.7 921 45 187 13.7 921 46 187.5 13.7 921 47 188 189 189 188 protein gealatin-binding 28K protein C:Accession: JC4708: JC4944 R:Maedd, K.; Okubo, K.; Shim Biochem. Biophys. Res. Communa, Title: CDNA cloning and exv A; Reference number: JC4708;
nn: JC47/8 s: 1-244 <mae> siterences: Duby: Desirences: Duby: Desirences: Duby: Desirences: Duby: Desirences: Duby: Desirences: Dube, T.; Ch. n. 120, 803-812, Isolation and chance number: JC4944 on: JC4944 on:</mae>	14.7 14.3 14.3 14.3 14.3 14.1 14.1 14.1 14.1 14.1 14.1 14.1 13.9 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.8 13.7
A; Accession: JC4708 A; Accession: JC4708 A; A; Cassidues: 1-244 < MAE> A; Cassidues: 1-246 < T; Choi-Miu J; Biochem. 120, 803-812, 1996 A; Mille: Isolation and character. A; Reference number: JC4944; MUID A; Accession: JC4944 A; Molecule type: protein is an endiction of the content of the	215 171 124 1315 1774 1774 1774 1774 1789 301 301 301 921 1464 289 193 375 1464 921 684 684 684 684 684 684 684 684 684 684
A; Accession: JC4708 A; Accession: JC4708 A; Accession: Lype: mRNA A; Residues: 1-244 < MAE> A; Cross-references: DDBJ.D45371; NID:g8718 A; Cross-references: DDBJ.D45371; NID:g8718 A; Choi-Miura, N.H.; l J. Blochem. 120, 803-812, 1996 A; Title: Isolation and characterization of A; Reference number: JC4944; MUID:97103474; A; Accession: JC4944 A; Molecule type: protein A; Residues: 19-38; 93-100;101-112;135-149;11 C; Comment: This protein is an endogenous f. C; Genetics: A; Genetics: A; Genetics: apM1 C; Superfamily: unassigned collagens; compl. C; Keywords: adipose tissue; glycoprotein; F; 1-18/Domain: signal sequence #status pre. F; 1-1-19/Tomain: complement C1q carboxyl-F; 95-M4/Product: gelatin-binding 28kba pre. F; 14-107/Region: collagen-like F; 14-107/Region: collagen-	30 201 14.7 215 2 C48150 31 197 14.4 171 2 A4443 32 196 14.3 224 2 A60032 33 195.5 14.3 1315 2 A56101 35 193.5 14.3 1774 2 B56101 35 193.5 14.1 296 2 A31219 36 193.5 14.1 296 2 A31219 37 193.5 14.1 921 2 S42617 39 192.5 14.1 921 2 S42617 40 190.5 13.9 289 2 T26817 40 190.5 13.8 193 2 A36812 41 189 13.8 193 2 A36812 42 189 13.8 193 2 A36825 43 189 13.8 193 2 S40495 44 187.5 13.7 921 2 S40495 45 187 13.7 684 2 A53019 RESULT 1 3C4708 3C4708 3C4708 3C4708 3C5 2C6
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IDN:BAA08227.1; PID: , T.; Tomita, M. 3, a novel gelatin-b 8947845 3 <nak></nak>	sr r r
IDN:BAA08227.1; PID:g87188 , T.; Tomita, M. 3 a novel gelatin-binding 8947845 1 clq carboxyl-terminal hom yproline 4 cSIG> 4 status experimental <mat <clo="" homology="" ral=""> tus experimental t) #status predicted DB 2; Length 244; T7; The lili </mat>	
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 104-112, 'X', 114-117;453-466 <NIN2>
C; Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl
C; Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl
C; Keywords: colled coil; extracellular matrix; glycoprotein; homotri
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F; 547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F; 453, 456/Modified site: hydroxyproline (Pro)-#status experimental
F; 611/Binding site: carbohydrate (Asn) (covalent) #status predicted
RESULT
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A;Residues: 'T',9',D',11-12,'EDOMKLYILFTM',30-31,'TCKSGRAFTTYMILQNVMADLVSSHT',48-89,'L'
629, 'PQAVLSLISMRTIKCGSSCQIQNPMVSIPLNMFILLSQVSYLLKSNNIPLTMS' <NIN1>
A;Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700
A;Accession: S77711
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A;Residues: I-674 <NINS
R;LuValle, P; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J. Biol. Chem. 263, 18378-18385, 1988
A;Title: The type X collagen gene. Intron sequences split the
A;Reference number: A31896; MUID:89054019; PMID:2461368 .
A;Accession: A31896
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A; Residues: 1-75 < LUV>
R; Ninomiya, Y; Gordon, M;
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C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S21397; A31896; S65594; S77711; I50218
R;Ninomiya, Y; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S22243
A; Accession: S23297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                     SFSGFL
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                                                                                                                                                                                                                                                            YVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN---GALHGDHQRFS 235
                                                                                                                                                                                                                                                                                                                   AFTVILSKAYPGATVPIKFDKILYNRQQHYDPRTGIFTCRIPGLYYFSYHV--HAKGTNV 604
                                                                                                                                                                                                                                                                                                                                                                 AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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30.9%; Pred. No. 2.30
tive 23; Mismatches
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; homotrimer; hydroxyproline
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A; Residues: 1-680 <KON>
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C; Species: Mus musculus (house mouse)
                                                                                                                                                                               Matches
                100 QHGPKGEKGYPGIP-
                                                                                                                                                                                                          Local
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                                                                                                                                                                               Conservative
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-12, F; 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mous A;Reference number: I48299; MUID:92267014; PMID:1587271
A;Accession: I48299
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: DNA
A;Residues: $2-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',
A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
R:Summers, T.A.; Irwin, M.H.; Mayne, R.; Ballan, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an ar A;Reference number: $26397; MUID:88087150; PMID:2826450
A;Accession: $26397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: collagen alpha l(VIII) chain; complement C1q carboxyl-terminal homolog C;Keyvords: coiled coil: extracellular matrix; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
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A;Title: Characterization of the mouse type X collagen gene A;Reference number: S30127; MUID:93261348; PMID:8492743
A;Accession: S30127
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A;Residues: 385-450,'K',452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1;
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A; Residues: 1-285, 'A', 287-680 <ELI>
                                                                                443 GEPGIPGTRGPTGPPGVPGFPGSKGDPGNPGAPGPAGIATKGLNGPTGPPGPPGPRGHSG 502
                                                                                                                                                                GDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATG----HEGAKGEKGDKGDLGPRGERG 99
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                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                 Score 278.5;
Pred. No. 3.
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-PELQ--
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-IAFMASLATHF 128
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Holecule type: mRNA
A;Residues: 1-246 <PET>
A;Cross references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229
A;Cross references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229
C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal homology <C1Q>
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S29328
R;Petry, F.; Reid, K.B.M.; Loos, M.
Eur. J. Biochem. 209, 129-134, 1992
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C;Superfamily: C;Keywords: coi
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A;Restdues: 1-674 <THO>
A;Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, Biochem. J. 273, 141-148, 1900. Biochem. J. 273, 140-148, 1900. Biochem. J. 273, 140-148, 1900. Biochem. J. 273, 141-148, 1900. Biochem. J. 273, 141-148, 1900. Biochem. J. 273, 141-148, 1900. Biochem. J. 273, 1900. Bi
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C; Species: Mus musculus (house mouse)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-
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C:Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
C:Accession: S13301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 72; Conser
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                                                                                                                                                                                                                                                                                                              PMID: 139669:
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A;RCESSEULE type: mRNA
A;ROlecule type: mRNA
A;Rosidues: 547-656 <RE2>
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A;Cross-references: GB:M74050; GB:D57494; NID:g53986; GB:D57494; NID:g53986; GB:D57494; NID:g57494; NID:g57494; NID:g57494; NID:g57494; NID:g57494; NID:g57494; NID:g57494; NID:g57494; NID:g57494; NID:g57494;
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
C;Accession: S26396; S30086; S15826; S18249; A43901; 151870; S21856
R;Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; FEBS Lett. 311, 305-310, 1992
A;Title: Genomic organization and full-length cDNA sequence of human collag. A;Reference number: S26396; MUID:93012005; PMID:1397333
                                                                                                                                                                                                                                                                                                                  A;Title: In situ hybridization studies on the expression of type X collagen A;Reference number: A43901; MUID:92077285; PMID:1743401 A;Accession: A43901
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, 1 Dev. Biol. 148, 562-572, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Cloning of human alpha-1(X) collagen DNA and localization of A;Reference number: S15826; MUID:91243838; PMID:2037056 A;Accession: S15826
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A; Cross-references: EMBL: X65120; NID: 923129
A; Note: the initial difference is probably due
R; Apte, S; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
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A;Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID:g30014
R;Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solome
Biochem. J. 280, 617-623, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1992 A; Reference number: $30085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S18249; A; Accession: S18249
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A; Residues: 1-680 < REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCHUID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-26, 'T', 28-680 <THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X68952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 GEKGYPGIP----PELQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 GTSGLPGDPGPRGPPGEPGVEGRYKQKHQSVFTVTRQTTQYPEANALVRFNSVVTNPQGH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 GCYGIPGMPGMPGAPGKDGHDGLQGPKGEPGIPAVPGTQGPKGQKGEPGMPGHRGKNGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GYQGPPGPPGPPGIPGNHGNNGNNGATGH-----EGAKGEKGDKGDLGPRGERGQHGPK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The human collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKSDTSSNHAVLKLAKGDEVWLRMG--NGALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSKQVSSGGALLRLQRGDEVWLSVNDYNGMV-GIEGSNSVFSGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNPSTGKFTCEVPGLYYFVY - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSM-----YSYEMK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X gene. Complete primary translated sequence and MUID:92109659; PMID:1764025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: X72578; EMBL: X72579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 274; DB 2;
Pred. No. 2.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IAFMASLATHFSNQNSGIIFSSVETNIGNF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTSHTANLCVHLNLNLARVASFCDHMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                      carboxyl-terminal doma
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A;Status: .......
A;Molecule type: mRNA
A;Residues: 520-597,'D',599-680 <WAL>
A;Residues: 520-597,'D',599-680 <WAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be important for skeletogenesis
C;Superfamily: collagen alpha 1(VIII) chain; co
C;Keywords: coiled coil; extracellular matrix;
F;1-18/Domain: signal sequence #status predicte
A; Experimental source: C; Genetics: A; Note: DKFZp586B0621.
                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <OTT>
                                                                                                                                                               submitted to the Protein S
A; Reference number: Z18184
A; Accession: T14782
                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C;Accession: T14782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia C; Complex: type X collagen may be a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60 A;Note: mutant sequence from patient with metaphyseal A;Note: a second mutant sequence with 614-Pro is also C;Comment: Prolines and lysines at the third position ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: structural component of extracellular fibrous polymer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 52/1
                                                                     A; Cross-references: EMBL: AL110261
                                                                                                                                                                                                                                       R;Ottenwaelder, B.; Obermaier,
                                                                                                                                                                                                                                                                                                                                   hypothetical protein DKF2p586B0621.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 6q21-6q22
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19-68/Domain: signal sequence #status predicted <MAT>
19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
19-65/Domain: anino-terminal nonhelical #status predicted <NC2>
57-519/Region: interrupted helical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGD----
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  DKF2p586B0621.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GN---GALHGDHQRFSTFAGFLL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLPGPVGPA--GAKGMPGHNGEAGPRGAPGIPGTRGPIGPPGIPGFPGSKGDPGSPGPPG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGIATKGLNGPTGPPGPPGPRGHSGEPGLPGPPGPPGPPGQAVMPEGFIKAGQRPSLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----IAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGV 162
                                                 adult
                                                                                                                                                                                                            Sequence
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28.5%;
                                                 uterus;
                                                                                                                                                                                                                                       В.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 270; DB 1;
Pred. No. 1.7e-14;
                                                                                                                                                                                                              Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           677
                                                                                                                                                                                                                                       Mewes, H.W.;
                                            clone DKFZp586B0621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                 August
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x; glycoprotein; homotrimer; hydro
                                                                                                                                                                                                                                       Gassenhuber,
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A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-744 <YAM>
A;Residues: 1-744 <YAM>
A;Residues: 1-746 = A;Cross references: GB.J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
A;Cross references: GB.J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
C;Superfamily: collagen alpha 1(VIII) chain; complement C1g carboxyl-terminal F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
F;21-117/Region: amino-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 264, 16022-16029, 1705
A;Title: The cloning and sequencing of alphal(VIII) collagen
Omains similar to those of type X collagen.
A;Reference number: A34246; MUID:89380199; PMID:2476437
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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F;572-744/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                       34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 PGPPGPPGIPGNHGN-----NGNNGATGHEGAKGEKGD-----KGDLGPRGERGQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                               AYHV--HCKGGNVMVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSE
                                                                                                                                                                                                                                                                                                                              GIPGD--QGLQGPPGIPGITGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGKPGVAGLHGP 543
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                                                                                                                       TFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN-
                                                                                                                                                                                                                                                                                     KGDKGDLGPRGERGQHGPKGEKGYPGIP-----
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QAAGLYAGQYVHSSFSGYLLY
                                        --GALHGDHQRFSTFAGFLLF
                                                                                                                                                              KKGKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYF
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carboxyl-terminal nonhelical
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Pred. No. 1.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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A; Residues:
C; Comment · m
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                                             A;Reference number: A90304; MUID:80020137; A;Accession: A03207
A;Molecula +---
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A; Residues: 1-245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, Eur. J. Biochem. 197, 615-622, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(VIII) chain precursor
A; Molecule type: protein
A; Residues: 29-56,'p',58-65,'K',67-71,'p',73-83,'K',85-86,'D',88-89,'N',91-122
C; Comment: The first component of complement is a calcium-dependent complex of
                                                                                                    Biochem. J. 179, 367-371, 1979
A; Title: Complete amino acid s
                                                                                                                                             R; Reid, K.B.M
                                                                                                                                                                                                                              A; Reference number: A; Accession: S14351
                                                                                                                                                                                                                                                A; Title: Characterization and organization A; Reference number: S14350; MUID:91174759;
                                                                                                                                                                                                                                                                                          Biochem. J. 274, 481-490, 1991
                                                                                                                                                                                                                                                                                                              R;Sellar, G.C
                                                                                                                                                                                                                                                                                                                                                                                             N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                              complement subcomponent Clq chain C precursor
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                                                                                                                                                                                                                                                                                                                                                ;Species: Homo sapiens (man);Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change
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21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>
21-117/Region: amino-terminal monhelical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: mRNA
;Residues: 1-744 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :Cross-references: EMBL:X57527; NID:g30081; PIDN:CAA40748.1; PID:g30082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession:
                                                                                                                                                                                                                                                                                                                             Accession: S14351; A03207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 AYHV--HCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 KKGKNGGPAYEMPAFTAELTAPFPPVGGPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNG-----NNGATGHEGAKGE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGDKGDLGPRGERGQHGPKGEKGYPGIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIPGD--QGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGKPGVAGLHGP 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --GALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                                                                                                                                                  1-245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S15435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                            ; Blake,
                                                                                                                        367-371,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                     <SEL>
                                                                                                                                                                                                                                                                                                                                                                                             complement subcomponent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFF
                                                                                                                                                                                                                                                                                                            D.J.; Reid, K.B.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 256.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-Jan-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                         translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 2.4e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                   the three collagen-like; PMID:486087
                                                                                                                                                                                                                                                                                                                                                                                           C1q
                                                                                                                                                                                                                                                  of the genes
PMID:1706597
                                                                                                                                                                                                                                                                                                                                                                                             gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B.R.; Ninomiya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELQI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 744;
                                                                                                                                                                                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                      22-May-1998
                                                                                                                                                                                                                                                                       the
                                                                                                      regions
                                                                                                                                                                                                                                                                     A-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                       8-
                                                                                                      present
                                                                                                                                                                                                                                                                     and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
    <REI>
                                                                                                                                                                                                                                                                         C-chain:
                                                                                                         'n
      thred
                                                                                                         sut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement subcomponent C1q chain B precursor [validated] - human N; Alternate names: complement subcomponent C1q beta chain C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) G; Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change 08-Dec-2000 C; Accession: B23422; A23422; B90304; A90301; B90315; A03206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   멍
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIHUQB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Reid; K.B.M.
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F;57,72,75/Modified site: 5-nyaroxyiys
F;75/Binding site: carbohydrate (Lys)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;31-114/Domain: collagenous, triple helix <COL>
F;121-244/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;121-244/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;32/Disulfide bonds: interchain #status experimental
F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline
F;57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: complement subcomponent C1q chain A; con C;Keywords: complement pathway; glycoprotein; homodime: F;1-28/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 60/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1p36.3-1p34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB:C1QG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;29-245/Product: complement subcomponent Clq chain B #status predicted
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ivation of Clr (enzyme), Cls (proenzyme), and the other eight components of cor;
Comment: The Clq subcomponent is composed of nine subunits, six of which are dimers of the C chain. Equimolar amounts of the A, B, and C chains are found a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                   148
                                                                             204
                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                 GNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTS 204
                                                                                                                                                                                                                                                                                                                                                                                                 PGMPGLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDK
                                                                                                                                                                                   QGDYDTSTGKFTCKVPGLYYFVYHA---SHTANLCVLLYRSGVKVVTFCGHTSK-TNQVN
                                                                                                                                                                                                                                                                                      GPMGPPGMPGVPGPMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVLTNP 147
                                                                                                                                                                                                                                                                                                                                          GDLGPRGERGQHGPKGEKGYPG----IPPELQIAFMASLATHF-SNQNSGIIFSSVETNI 144
                                                                                                                              SNHAVLKLAKGDEVWLRMGN-----GALHGDHQRFSTFAGFLLF
                                                                          SGGVLLRLQVGEEVWLAVNDYYDMVGIQGSD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDB:128132;
                                                                                                                                                                                                                                                                                                                                                                                                 GAPGKDGYDGLPGPKGEPGIPAIPGIRGPKGQKGEPGLPGHPGKN 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMIM: 120575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 255; DB 1
Pred. No. 1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (covalent) #status experimental
                                                                               -SVFSGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement Clq carboxyl-terminal imer; hydroxylysine; hydroxyprolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 245
                                                                               243
                                                                                                                                 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Pro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
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Biochem. J. 231, 729-735, 1985
A;Title: Molecular cloning and characterization of the complementary DNA and A;Reference number: A23422; MUID:86076906; PMID:3000358 A; Note: the authors translated A; Accession: A23422 A; Molecule type: DNA A; Residues: 'HS',1-32 <REI> A; Accession: B23422 the codon AGT for the second position as Arg; they gene cod wei

A; Molecule type: mRNA

A; Residues: 28-253 <RE1> A; Cross-references: EMBL:X03084 A; Note: the authors translated the codon ACA for residue 46 as

R; Reid, K.B.M. Biochem. J. 179, 367-371,

A; Reference number: A; Title: Complete amino 7-371, 1979 mino acid sequences of A90304; MUID:80020137; the three collagen-like; PMID:486087 regions present

in

A; Accession: B90304

A; Molecule type: protein A; Residues: 'E.29-84,'D', 86-99,'P',101-135 R; Reid, K. B.M.; Thompson, E.O.P. Biochem. J. 173, 863-868, 1978

A:Title: Amino acid sequence of the N-terminal 108 amino A;Reference number: A90301; MUID:79041552; PMID:708376 A;Accession: A90301 acid residues of. the В

protein

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RESULT 12
S23298
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A;Rosidues: 136-253 <RE4>
A;Rosidues: 136-253 <RE4>
A;Rosidues: 136-253 <RE4>
A;Note: 176-Glx may also be present
C;Comment: The first component of complement is a calcium-dependent complex of the three ivation of Clr (enzyme), Cls (proenzyme), and the other eight components of complement.
C;Comment: The Clq subcomponent is composed of nine subunits, six of which are disulfide (see PIR:C1HUQC) chain. Equimolar amounts of the A, B, and C chains are found after redu
ρ
                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-744 <NIN>
                                                                                                                                                                                                                                                                                                                                              in Extracellular Matrix Genes, A; Title: The molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                      R;Ninomiya, Y.; Castagnola, P.; maguchi, N.; Olsen, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(VIII) chain - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;28-253/Product: complement subcomponent C1q chain B #status experimental <MAT>F;33-116/Domain: collagenous, triple helix <COL>F;33-249/Domain: complement C1q carboxyl-terminal homology <C1Q>F:123-249/Domain: complement C1q carboxyl-terminal homology <C1Q>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 1p36.3-1p34.1
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hom
C;Reywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline
F;1-27/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                               A; Accession: S23298
                                                                                                                                                                                                                                                                                                                     A; Reference number: S22243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 203, 559-569, 1982
A;Title: Completion of the amino acid sequences of the A and B chains of subcomponent A; Fixed e number: A90315; MUID:82283890; PMID:6981411
A; Accession: B90315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GDB:119043; OMIM:120570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:C1QB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                            Superfamily: col 617-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 CHGDYSFRGYQGPPGPPGP---PGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERG
  3
4
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K.B.M.; Gagnon, J.; Frampto
. J. 203, 559-569, 1982
                                                                                Local
GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEMKGKSDTSSNHAVLKLAKGDEVWLR-MGNGALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFFDVMTGRFGAPVSGVYFFTFS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTINVPLRRDQTIRFDHVITNMN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QHGPKGEKGYPGIP------PELQIAFMASLATHFS-NQNSGIIFSSVETNIG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGPPAIPGIPGIPGPPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNPGKVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNYEPRSGKFTCKVPGLYYFTYHASSRGNLCVNLMRGRERAQKVVTFCDYAYNTF----
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              S23298
                                                                                                                                                         collagen alpha 1(VIII) chain; complement Clq carboxy1-terminal homology
in: complement Clq carboxy1-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QVTTGGMVLKLEQGENVFLQATDKNSLLGMEGANSIFSGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%;
31.7%;
                                                                              18.4%;
29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frampton,
                                                                                                                                                                                                                                                                                                                                                 Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Proof collagens with short triple-helical domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerecke,
                                                                           Score 251.5;
Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 251.5; DB 1;
Pred. No. 2.1e-13;
Pred. No. 289;
                                            Pred. No. 6.26
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J
                                                                                                                                                                                                                                                                                                                                                                                                                               D.;
                                                                           6.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MMKHEDVEEVYVYLMHNGNTVFSMYS
                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon, M.K.;
                                                                                                       DB 1;
                                                     104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                     Indels
                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                               Jacenko,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                     55;
  KGE 85
                                                                                                                                                                                                                                                                                                                                                                                                                            O.; LuValle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A57131; MUID:91210292; PMID:2019595 A;Accession: A57131
                                  Qy
                                                                              DЬ
                                                                                                                                                                 DЬ
                                                                                                                                                                                                                                               Дb
                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R. J. Biol. Chem. 266, 7721-7727, 1991
A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
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                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A57131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen alpha 2(VIII) chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1p34.3-1p32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:127812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: COL8A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-635 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
629
                                                                                  570
                                                                                                                                                                   514
                                                                                                                                                                                                          125
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                                         239
                                                                                                                                                                                                                                                                                           105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 GIPGD--QGLQGPPGIPGITGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGKPGVAGLHGP 543
                                                                                                                                                                                                                                                                                                                                  395 GPSGIPGLQGPAGPIGPQGLPGLKGEPGLPGPPG-EGRAGEPGTAGPRGPPGVPGSPGIT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 KKGKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYF
                                                                                                                                                                                                                                                                                                                                                                            45 GDYSFRGYQGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                         GFLLFET 245
                                                                                YKNNVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQIPSDQANG-LYSTEYIHSSFS
                                                                                                                       NGNTVFSMYSYE--MKGKSDTSSNHAVLKLAKGDEVWLRM----GNGALHGDHQRFSTFA 238
                                                                                                                                                                                                      ATHESNONSGIIESSVETNIGNEEDVMTGREGAPVSGVYEETESMMKHEDVEEVYVYLMH
                                                                                                                                                                                                                                                                                           GEKGYPGIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAAGLYAGQYVHSSFSGYLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYHV--HCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQNPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGDKGDLGPRGERGQHGPKGEKGYPGIP-----PELQI----
GFLLCPT
                                                                                                                                                                 TSPLPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAY----HVHVKGTNVWVAL
                                                                                                                                                                                                                                                  GPPGLPGPPGAPGAFDETGIAGLHLPNGGVEGAVLGKGGKPQFGLGELSAHATPAFTAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPAPQGEYLPDMGLGIDGVKTPHAYAA
                                                                                                                                                                                                                                                                                                                                                                                                                     76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:M60832; NID:g177178; PIDN:AAA62822.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                       18.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 249; DB 2; Pred. No. 8.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                           ------PELQI------AFMASL 124
                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     52;
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                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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collagen alpha 1(VIII) chain

mouse

RESULT 14 S23779

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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S23779
R;Muragqki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y. Eur. J. Biochem. 207; 895-902, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polypept A;Reference number: S23779; MUID:92362626; PMID:1499564 A;Accession: S23779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement subcomponent C1q chain A precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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A; Residues: 1-743 < MUR>
                                                                                                                                                                                                                                                                            QΥ
B
                                                  Qy
                                                                                                           В
                                                                                                                                                             δÃ
                                                                                                                                                                                                                         망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 147, 3988-3993, 1991
A;Title: Gene expression of the A- and B-chain of mouse Clq in different tissues and the A;Reference number: S19018; MUID:92043789; PMID:1940381
A;Accession: S19018
                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;116-243/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-245 <PET>
A; Residues: 1-245 <PET>
A; Cross-references: EMBL: X58861; NID: 950226; PIDN: CAA41664.1; PID: 950227
C; Superfamily: complement subcomponent C1g chain A; complement C1g carboxyl-terminal hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Petry, F.; Reid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                722 AAGLYAGQYVH-SSFSGYLLY 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 664 YHV--HCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQNPFEQ 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLR-----M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 KGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFA 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKTPHAYAGK 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 GIPGD--QGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGKPGVAGLHGP 543
150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 GNGALHGDHQRFSTFAGFLLF 243
                                                  154 RFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG--NTVFSMYSYEMKGKSDTSSNHAVLK 211
                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 KGDKGDLGPRGERGQHGPKGEKGYPGIP------PELQI------ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGPPGNHGNNGNNGATGHEGA------KGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
mes 77; Conserv
                                                                                                                                                                                                                            31
                                                                                                                                                                                                                                                       51 GYQGPPGPPGIPGNHGNNGNNGATG-HEGAKGEKGDKGD------LGP 94
RFICAVPGFYYFNFQVISKWDL-CLFIKSSSGGQPRDSLSFSNTNNKGLFQVLAGGTVLQ 208
                                                                                                           LGDSGPQGLKGVKGNPGNIRDQPRPAFSAIRQNPMTLGNV-VIFDKVLTNQESPYQNHTG 149
                                                                                                                                                                RGERGOHGPKGEKGYPG-IPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTG 153
                                                                                                                                                                                                                            GKDGAPGNPGRPGLKGERGEPGAAGIRTGIRGFKGDPGESGPPGKPGNVGLPGPSGP 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.B.M.; Loos, M.
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                                                                                                                                                                                                                                                                                                                                                                     17.5%; Score 239.5; DB 2 33.2%; Pred. No. 1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                          26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102; Indels
                                                                                                                                                                                                                                                                                                                                          94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 245;
                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                     InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 2.
                                                                        EMBL; AF329839; AAK17963.1; -. EMBL; BC022187; AAH22187.1; -. Genew; HGNC:14342; ClQTNF7.
                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1367;
Pred. No. 1
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RESULT 3
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Best Local
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DOMAIN
SEQUENCE
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Collagen;
SIGNAL
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SEQUENCE FROM N.A.
Piddington C.S., Bishop P.;
"Homo sapiens complement-ciq tumor necrosis factor-related
"Homo sapiens complement ciq tumor necrosis factor-related
     EMBL; BC011699; AAH11699.1; Genew; HGNC:14325; C1QTNF2. Interpro; IPR001073; C1q.
                                                                                                                                                           This
                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                     Complement-clq tumor necrosis factor-related protein ClQTNF2 OR CTRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BxJ̄5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                  EMBL; AF329836; AAK17960.1;
EMBL; BC011699; AAH11699.1;
                                                                            or send an email to license@isb-sib.ch).
                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                    use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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                                                                                                                                                                                                                                         FISSUE=Muscle;
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                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a
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                                                                                                                                           the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS01113; C1Q; 1.
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Pred. No. 1.3e-1
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                              Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                    Usage
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                                                                                                                                             EMBL outstation
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IPR000087;

Collagen

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RESULT 4
C1RF_HUMAN
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C1RE_HUMAN 51....

C75973;

16-OCT-2001 (Rel. 40, Created)

T 16-OCT-2001 (Rel. 40, Last sequence updated)

T 16-OCT-2002 (Rel. 41, Last annotation up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                        MEDLINE=99097000, .... Bertram M.J., naccase Berube N.G., Swanson X.H., Bertram M.J., naccase Baskin D.S., Smith J.R., Pereira-Smith O.M.;
Baskin D.S., Smith J.R., Pereira-Smith O.M.;
"Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, a novel Clq-related factor, "Cloning and Characterization of CRF, "Cloning and Characterization of CRF, "Clo
            Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases -!- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. -!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN. -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                 Strausberg R.;
                                                                                                                      TISSUE=Placenta;
                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                     Nickerson
Submitted
                                                                                                                                                                                                                              Rieder
                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=99097006; PubMed=9878755;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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SMART; SM00110; C1Q;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATHESNQNSGIIFSSVETNIGNEFDVMTGREGAPVSGVYFFTFSMM---KHEDVEEVYVY
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PF01391; Collagen;
                                                                                                                                                                                                                              М.J.,
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                                                                                                                                                                                                          D.A.;
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29952
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Primates;
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285
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                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
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; 7E31FF9868D4EDFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 304; DB 1; Pred. No. 1.1e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELATED PROTEIN 2. COLLAGEN-LIKE.
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
                                                                                                                                                                                                                       Chung M.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
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RESULT 5
C1RF_MOUSE
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InterPro; IPRO00087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                              C1RF_MOUSE
088992;
                                                                                                                                                                                                                                                                      16-OCT-2001
16-OCT-2001
         "Cloning and characterization of CRF, a novel Clq-related factor, expressed in areas of the brain involved in motor function."; Brain Res. Mol. Brain Res. 63:233-240(1999).

-!- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT IN AREAS OF THE NETWOOD SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS THE PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUCLEUS, THE PONS AND THE RED NUCLEUS.

-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
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DOMAIN
DOMAIN
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 1 1
                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                            Clorf or crf.
                                                                                                                                                                                                                                                          Clq-related factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                      Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko Baskin D.S., Smith J.R., Pereira-Smith O.M.;
                                                                                                                                              MEDLINE=99097006; PubMed=9878755;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                   16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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258 AA;
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1 (Rel. 40,
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CONTAINS 1 COLLAGENOUS CONTAINS 1 C1Q DOMAIN.
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258
115
258
                                                                                                                                                                                                                                                          precursor
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Rodentia;
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                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                 Created)
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Pred. No. 3.
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                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                              PRT;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APM1_MOUSE S'
Q60994; Q62400; (
Q1-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Createw, 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Adiponectin precursor (30 kDa adipocyte complement-related Adiponectin AdipoQ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                TISSUE-Adipocyte;
MEDLINE-96070757; PubMe
Scherer P.E., Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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   MEDLINE=96209999;
Hu E., Liang P., :
                                                                 TISSUE=Fibroblast;
                                                                                                                                                                                               adipocytes.";
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
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                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                      "A novel serum protein
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                                                                                                                                                              Biol. Chem.
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n; PF01391; Collagen; 1.
TTS; PR00007; COMPLEMNTC1Q.
TTS; SM00110; C1Q; 1.
SITE; PS01113; C1Q; 1.
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      Spiegelman
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                                                                                                                                                                                                                                                                                    PubMed=7592907;
                             PubMed=8631877;
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C1Q-RELATED FACTOR.
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C1Q.
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Sciurognathi; Muridae;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,
RA Aitawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Hleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21372499; PubMed=11479628; Berg A.H., Combs T.P., Du X., Brow
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Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N.,
Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., I
Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kir
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J. Biol. Chem. 271:10697-10703(1996).
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ween the Swiss Institute.
European Bioinformatics Institute.
by pon-profit institutions as lifted and this statement is not remained and the statement and the statement is not remained and the statement is not remained.
                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: SECRETED I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITS ENDOTHELIAL NE-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS THE-ALPHA-INDUCED
                                                                                                                                                                                                                                                                                                                                  SECRETED INTO SERUM. INDUCTION: DURING HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. CONTROL OF FAT METABOLISM AND INSULIN SENSITI SUBUNIT: HOMOOLIGOMER.
                                                                                                                                                                                                                                                                          SIMILARITY:
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Fukuda S.,
manaka I.,
Saito R.,
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Best Local
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Adiponectin
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APM1_HUMAN
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SEQUENCE
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      binding protein).
APM1 OR ACRP30 OR GBP28.
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Pfam; PF01391; Collagen; 1.
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                          (ACRP30) (Adipose most abundant
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                                                                                                                              LYADNVNDSTFTGFLLY 243
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                                                                                                                                                                                                     EAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHIT
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sapiens
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SM00110; C10; 1.
E; PS01113; C1Q; 1.
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243
247
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                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
precursor (30 kDa adipocyte complement related
                                                                                                                                                                                                                                                                                                                    Conservative
(Human)
                                                                                  STANDARD;
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M -> V.
P -> S (IN REF
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A -> G (IN REF
G -> N (IN REF
Y -> F (IN REF
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Pred. No. 6.5e-18;
0; Mismatches 102
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COLLAGEN-LIKE.
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                           gene
                           transcript 1) (apM-1)
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VARIANTS ARG-84; MET-117; THR-164; SER-221 MEDLINE=21671103; PubMed=11812766; Hara K., Boutin P., Mori Y., Tobe K., Dina Otabe S., Okada T., Eto K., Kadowaki H., Ha
                                                                                                                                                                                                                                                                                                                                                                                                          Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H., Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y., Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.; "Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF-kappaB signaling through a cAMP-dependent pathway."; Circulation 102:1296-1301(2000).
                                                                                              adiponectin.";
                                                                                                                              Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K.
Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nal
Yamashita S., Funahashi T., Matsuzawa Y.;
                                                                                                                                                                              VARIANT ADIPONECTIN DEFICIENCY CYS-112. MEDLINE-20378830; PubMed=10918532;
                                                                                                                                                                                                                     Nat.
                                                                                                                                                                                                                                                                              Froguel P., Kadowaki T.;
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Shudo K., Yoda M., Nakano Y.,
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Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N.,
Akanuma Y., Gavrilova O., Vinson C., Reitman M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
MEDLINE=20440368; PubMed=10982546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Adiponectin, a new member of the family of soluble defense collagens, negatively regulates the growth of myelomonocytic progenitors and the functions of macrophages.";
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Yokota T., Oritani K., Takahashi I., Ishikawa J
Ouchi N., Kihara S., Funahashi T., Tenner A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 1q21.3-q23, a susceptibility locus identified combined hyperlipidemia (FCH)."; biochem. Biophys. Res. Commun. 260:416-425(1999).
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Nakano Y., Shimizu N., Tomita M.;
"Organization of the gene for gelatin-binding
Gene 229:67-73(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Adipose tissue;
MEDLINE=96224171; Pubm
Maeda K., Okubo K., Sh
                                                                                                                 "Genomic structure and mutations
                                                                                                                                                                                                                                                associated
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                                                                                                                                                                                                                                                                                                                                                                               FUNCTION
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MEDLINE-99196984; PubMed=10095105;
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"CDNA cloning and expression of a nover wearer."
"CDNA cloning and expression of a nover wearer."
"AdiPose Most abundant Gene transcript 1).";
factor, apm1 (AdiPose Most abundant Gene transcript 1).";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     8
                                                                                                                                                                                                                             Med. 7:941-946(2001).
                                                                                                                                                                                                                                       fat-derived hormone adiponectin reverses insulin resistance clated with both lipoatrophy and obesity.";
                                                                                 Relat.
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Y., Tobe K., Nagai R., Kimura
                                                                                  Disord.
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                                                                                 24:861-868(2000)
                  Dina C.,
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Hagura
                                                  AND PRO-241.
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Yasuda K., Y.
a R., Akanuma
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Kimura S.,
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.

-i- SUBURIT: HOMOOLIGOMER (POTENTIAL).
-i- SUBCELULAR LOCATION: SECRETED IN PLASMA.
-i- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.
-i- DISEASE: Defects in APMI are the cause of adiponectin deficiency, resulting in very low concentration of plasma adiponectin. Decreased adiponectin plasma levels are associated with obesity insulin resistance, and diabetes type 2.
                                                                                                                                                                                                                MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                          SMART; SMULLEY, 1.—210; 1.

PROSITE; PSO1113; C10; 1.

Hormone; Collagen; Signal; Repeat; Hydroxylation; Hormone; Collagen; Signal; Repeat; Hydroxylation; Hormone; Collagen; Signal; Repeat; Hydroxylation; Obesity; Diabetes
                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB012165; BAA86716.1; -.
EMBL; AB012164; BAA86716.1; JOINED.
EMBL; AJ131460; CAB52413.1; -.
EMBL; AJ131461; CAB52413.1; JOINED.
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Pfam; PF01391; Collagen; 1.
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 SEQUENCE
                                                                                VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yazaki Y., Nagqi R., Taniyama M., Matsubara K., Yoda M., Nakano Y., Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.; "Genetic variation in the gene encoding adiponectin is associated with increased risk of type 2 diabetes in the Japanese population.":
                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Piddington C.S., Sheppard P.O

"Homo sapiens complement-clq
Submitted (DEC-2000) to the E
                CARBOHYD
                                                             DOMAIN
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                                                                                                                                                 Collagen;
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                                                                                                                                                                                                                                                                                      InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COmplement-clq to
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                                                                                                                                                                           PROSITE; PS01113; C1Q;
                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
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-1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 TGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNH 142
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                                                                                                                                                                                                                                                                                                                                 BC020551; AAH20551.1;
; HGNC:14343; ClQTNF6;
                                                                                                                                                                                                                                                                                                                                                                                AF329842; AAK17966.1; -.
                                                                                                                                                                                                   SM00110; C1Q;
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el. 41, Last annotation update)
tumor necrosis factor-related
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Pred. No. 7.1e
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                                                           RELATED PROTEIN COLLAGEN-LIKE.
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16-OCT-2001 (Rel. 40
15-JUN-2002 (Rel. 41
Gliacolin precursor.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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J.
       DOMAIN
SEQUENCE
                                                                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: EXPRESSED IN GLIAL CELLS.
-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koide T., Aso A., Yorihuzi T., Nagata K.;
"Conformational requirements of collagenous peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20428709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLIC_MOUSE
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                                                                                                                                                                                                            Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen; 1.
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                                                                                                SIGNAL
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Biol. Chem. 275:27957-27963(2000).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation on its
                                                                                                                <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                 Luvalle P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;
"The type X collagen gene. Intron sequences split the 5'-untranslated region and separate the coding regions for the non-collagenous aminoterminal and triple-helical domains.";
J. Biol. Chem. 263:18378-18385(1988).
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01-NOV-1991 (Rel. 20,
15-JUL-1999 (Rel. 38,
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                                                              PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS. SIMILARITY: CONTAINS 1 C10 DOMAIN.
                                                                                                                                                          Siol. Chem. 264:16022-16029(1989).
FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
                                                                                                                                MINERALIZATION ZONES OF HYALINE CARTILAGE. SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   developmentally regulated type X reading frame without introns."; iol. Chem. 261:5041-5050(1986).
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modified
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01-NOV-1995 (Rel. 32, Last seq
01-NOV-1995 (Rel. 32, Last anno
Collagen alpha 1(X) chain prec
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Elima K., Berola I., Rosati R., Metsaranta M., G
de Crombrugghe B., Vuorio E.;
"The mouse collagen X gene: complete nucleotide
structure and expression pattern.";
                                                                                                            STRAIN-BALB/c;
MEDLINE=93143676;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q05306;
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Pfam; PF01391; Collagen; 8
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InterPro; IPR000087; Collagen
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EMBL; J04194; AAA48634.1;
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SM00110; C1Q; 1.
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                                                                                                               PubMed=8424763;
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                                                                                                                                                                                                                                                          Muridae;
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Elima K., Wetsacranta M., Kallio J., Peraelae M.
Garofalo S., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse alpha 2.
collagen mRNAs."
Biochim. Biophys. Acta 1130:78-80(1992).
-i-FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYI
CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRES
MINERALIZATION ZONES OF HYALINE CARTILAGE.
-i-SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X67348; CAA47763.1; -. EMBL; X65121; CAA46237.1; -. EMBL; X63013; CAA44741.1; -. EMBL; Z21610; CAA79736.1; -. PIR; S28807; S28807. S28807. S21216. S31216.
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DOMAIN
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                                                                                                                                                                                                                                                                PRINTS; PRO0007; COMPLEMNTC10.
ProDom; PD000007; Collagen; 2.
SMART; SM00110; C1Q; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.;
*Cloning of the human and mouse type X collagen
the mouse type X collagen gene to chromosome 10.
Eur. J. Biochem. 206:217-224(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Intron-exon structure, alternative use of promoter and the mouse collagen X gene, Coll0a-1.";
Eur. J. Biochem. 213:99-111(1993).
                                                                                              DOMAIN
                                                                                                              DOMAIN
                                                                                                                                     DOMAIN
                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                         Cartilage; Collagen;
                                                                                                                                                                                                                                                                                                                            Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by are entities requires a license requires req
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MEDLINE=93238750;
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CONFLICT
                                                                                                                                                                                                                                  Extracellular matrix;
                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                             S22215;
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C1Q.
P ->
A ->
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T ->
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PRINTS; PR00007; COMPLEMNTC1Q. ProDom; PD000007; Collagen; 1.

Pfam; PF01391; Collagen;

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Best Local
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EMBL; X53550; C. PIR; S13301; S13301. InterPro; IPR001073; C1q. Theorpro; IPR000087; Col!
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01-NOV-1991
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                             TISSUB=Cartilage;
MEDLINE=9113131; PubMed=1703407;
Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                            Biochem. J. 273:141-148(1991).

- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                 collagen genes."
                                                                                                                                                                                                                                                                                                           "Isolation of cDNAs encoding the complete sequence of bovine type collagen. Evidence for the condensed nature of mammalian type {\tt X}
                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
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                                                                                                                                                                                                                                  SUBUNIT: HOMOTRIMER.
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                                                                       non-profit institutions as long d and this statement is not removed s requires a license agreement (See an email to license@isb-sib.ch).
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          Collagen
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RESULT 13
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STRAIN=BALB/C; TISSUE=Liver;

MEDLINE=96186528; PubMed=8606057;

Petry F., McClive P.J., Botto M., Morley B.J., Mo:
"The mouse C1q genes are clustered on chromosome of gene organization.";

Immunogenetics 43:370-376(1996).
-i- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES of C1, THE FIRST COMPONENT OF THE SERUM COMPLEME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993
01-JUL-1993
16-OCT-2001
                                                                                                                                                                                                                    MEDITNE-YSULTIO, FUNCTIONS M.;
Petry F., Reid K.B.M., LOOS M.;
"Isolation, sequence analysis and characterization of cDNA clones coding for the C chain of mouse Clq. Sequence similarity of coding for the C chain of mouse Clq. Sequence vinitarity of coding for the C chain of mouse Clq. Sequence similarity of coding for the C chain of mouse coding for the C chain of
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                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-Macrophage;
MEDLINE-93011118; PubMed=1396691;
                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
NCBI_TaxID=10090;
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InterPro; IPR000087; Collagen
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European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROENTME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
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                                                                      FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSM------
                                                                                                            GTSGLPGDPGPRGPPGEPGVEGRYKQKHQSVFTVTRQTTQYPEANALVRFNSVVTNPQGH
NSKQVSSGGALLRLQRGDEVWLSVNDYNGMV-GIEGSNSVFSGFLLF
                          GKSDTSSNHAVLKLAKGDEVWLRMG--NGALHGDHQRFSTFAGFLLF 243
                                                      YNPSTGKFTCEVPGLYYFVY
                                                                                                                                     GEKGYPGIP-----PELQ------IAFMASLATHFSNQNSGIIFSSVETNIGNF
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X92960; CAA63535.1;
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"Mutations in fibrillar collagens (type associated collagen (type IX), and net cause a spectrum of diseases of bone, Hum. Mutat. 9:300-315(1997).
                                                                                                                                                                                                                                                                                                             Apte S.S., Seldin M.F., Hayası. ... X collagen "Cloning of the human and mouse type X collagen gene to chromosome 10.
                                                                                                                                                                                                                                       MEDLINE=91243838; PubMe Apte S., Mattei M.-G., "Cloning of human alpha COL10A1 gene to the q21
        VARIANTS SMCD ASP-598 AND PRO-614.
MEDLINE=94136476; PubMed=8304336;
Meallis G.A., Rash B., Sweetman W.A.,
                                                                                                                                                          MEDLINE=92077285; PubMed=1743401; Reichenberger E., Aigner T., von "In situ hybridization studies on in fetal human cartilage.";
                                                                                                                                                                                                                            FEBS Lett.
                                                                                                                                                                                                                                                                                                          the mouse type X collagen gene to cl
Eur. J. Biochem. 206:217-224(1992).
                                                                                                                                                                                                                                                                                                                                           MEDLINE=92267014; PubMed=1587271; Apte S.S., Seldin M.F., Hayashi M.
                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The human collagen X gene. Complete primary translated sequence chromosomal localization."; Biochem. J. 280:617-623(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas J.T., Cresswell C.J., Rash B., Solomon E., Grant M.E., Boot-Handford
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Mammalia; Eutheria;
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16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                              MEDLINE=97255959; PubMed=9101290;
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43838; PubMed=2037056;
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"Novel missense mutation resulting in the substitution of ty cysteine at codon 597 of the type x collagen gene associated Schmid metaphyseal chondrodysplasia.";

J. Hum. Genet. 43:259-261(1998).

I. FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zabel B., Wynne-Davies R., Grant M.E., Boot-Handford R.P.;
"Mutations within the gene encoding the alpha 1 (X) chain of type collagen (COL10A1) cause metaphyseal chondrodysplasia type Schmid not several other forms of metaphyseal chondrodysplasia.";
J. Med. Genet. 33:450-457(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mutation of the type X collagen gene 'COL10A1' causes spondylometaphyseal dysplasia."; Am. J. Hum. Genet. 63:1659-1662(1998).
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Biol. Chem. 270:4558-4562(1995).
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MEDLINE=99069781; Pul
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McIntosh I., Abbott M.H., Warman M.L., Olsen B.R.
"Additional mutations of type x collagen confirm
Schmid metaphyseal chondrodysplasia locus.";
Hum. Mol. Genet. 3:303-307(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sawai H., Ida A., Nakata Y., Koyama K.;
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MEDLINE=99057503; PubMed=9837818;
Ikegawa S., Nishimura G., Nagai T.,
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MEDLINE-95331767; PubMed-7607655;
Bonaventure J., Chaminade F., Maroteaux P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      occur in two
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SUBUNIT: HOMOTRIMER.

SUBUNIT: HOMOTRIMER.

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. DISEASE: DEFECTS IN COLIOAI ARE THE CAUSE OF SCHMID TYPE METAPHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED DISORDER OF THE OSSEOUS SKELETON. THE CARDINAL FEATURES OF THE PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GAIT. RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, FLARING OF THE RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, ESPECIALLY OF THE METAPHYSES, AND A WIDE IRREGULAR GROWTH PLATE, ESPECIALLY OF THE
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DISBASE: DEFECTS IN COL10A1 ARE THE CAUSE OF SPONDYLOMETAPHYSEAL DYSPLASIA (SMD). SMD COMPRISES A HETEROGENEOUS GROUP OF HERITABLISELETAL DYSPLASIAS CHARACTERIZED BY MODIFICATIONS OF THE SKELETAL DYSPLASIAS OF THE SPINE AND METAPHYSES OF THE TUBULAR BONE VERTEBRAL BODIES OF THE SPINE AND 2 TYPE VIII COLLAGENS.
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Sheppard P.O., Humes J.M.;
"Homo sapiens complement-olg tumor necrosis factor-related protein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CQT5_HUMAN STANDARD; PRT; 243 AA.
Q9BXJO; Q9UFX4;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-clq tumor necrosis factor-related protein 5 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF329841; AAK17965.1;
EMBL; AL110261; CAB53702.1;
Genew; HGNC:14344; C1QTNF5.
InterPro; IPR001073; C1q.
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                                                                                                                                                                                                                                                                    SEQUENCE
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SMART; SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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TISSUE=Uterus;
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                                                    15 GSPPLDDNKIPSLCPG---HPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRP
                                                                             34 GLPP-DCSK---CCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGATGHEGAKGE----
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--KGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAFMASLATHFSNQNSGIIFSSVETN 143
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COMPLEMENT-CLQ TUMOR NECROSIS FACTOR-
RELATED PROTEIN 5.
COLLAGEN-LIKE.
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Search completed: January 15, 2003, 19:38:01 Job time: 40 secs

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                   O8r002 mus musculu

O96007 homo sapien

O962v4 mus musculu

O921s8 mus musculu

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                                                                      Q8te71 homo sapien
Q9z1k4 rattus norv
Q9h667 homo sapien
Q8tej5 homo sapien
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Q95mq4 bos taurus
Q95jd7 macaca mula
Q9n178 sus scrofa
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Q9dcm6 mus musculu
Q9qxp7 mus musculu
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ALIGNMENTS

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RA Arakawa T., Hara A., Fukunishi Y., Konnon H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., King B., Kochiwa H.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesolè G., Quackebbush J.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Bofielli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Ra Gustincich S., Hill D., Mashima J., Mamezarelli J., Mombaerts P.,
Ra Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ra Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Ra Aynshaw-Poris A. Yoshida K., Hasegawa Y. Kawaii H. Kohtsuki S.
                                                                                                                                                   Query Match
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STRAIN=C57BL/6J; TISSUE=PANCREAS;
MEDLINE=21085660; PubMed=11217851
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1810033K05RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1810033K05Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
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10
                                                              6 LIYWQLLALFFLPFCLCQDEYM-----ESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLFETK 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
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MISWVLLAC-ALP---CAADPMLGAFARRDFQKGGPQLVCS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLFETK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                                                                                                                                       Similarity
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                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-11217851;
                                                                                                                                                       22.9%;
28.9%;
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17,
17,
                                                                                                                      41;
                                                                                                                      Score 313; DB 11;
Pred. No. 3.8e-20;
41; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                      6D3905AE7C19E6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
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LPGPQGPP 54
                                                                                                                   82; . Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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RESULT 4
Q95JD7
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Best Local
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InterPro; IPR000087; Collagen.
InterPro; IPR000087; Collagen.
InterPro; IPR000087; Collagen: 1.
Pfam; PF01391; Collagen; 1.
ProDom: PD000007; Collagen: 1.
PROSITE; PS01113; Cl0; UNKNOWN_1.
SEQUENCE 240 AA; 26091 MW; C6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95MQ4
Q95MQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein, Adipo 0.";
J. Biol. Chem. 276:28849-28856(2001).
EMBL; AF269230; AAKS8902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;
"Identification and Adipocyte Differentiation-dependent Expression
the Unique Disialic Acid Residue in an Adipose Tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21369933;
Sato C., Yasukawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
Adipose tissue-specific protein adipo Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                 191
                                                                                                203
                                                                                                                                133
                                                                                                                                                                 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 RIRTFDANTGNHDVASGSTILALKEGDEVWLQIFYSEQNGLFYDPYWTDSLFTGFLIY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
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                                                                                                                                                                                                                                                                                  HGDYSFRGYQGPPGPPGP-----PGIPGNHGNNGNNGATGHEGAKGEKGDKGD---LGPR
                                                               QASGSVLLHLEVGDQVWLQVYEGENHNGVYADNVNDSTFTGFLLY
                                                                                         TSSNHAVLKLAKGDEVWLRMGNGALH----GDHQRESTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMM---KHEDVEEVYVYLMHNGNTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPPGIPGNHGNNGNNGATGHEGAKGEKGDKGD----
                                                                                                                                                               NIGNEFDVMTGREGAPVSGVYFETESMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSD
                                                                                                                                                                                                 GETGDVGMTGAEGPRGFPGTPGRKGEPGEAAYVYRSAFSVGLETRVTVPNVPIRFTKIFY 132
                                                                                                                                                                                                                               GER----GQHGPKGEKGYPGIPPE------LQIAFMASLATHFSNQNSGIIFSSVET 142
                                                                                                                                                                                                                                                               HGEDNM----EDPPLPKGACAGWMAGIPGHPGHNGTPGRDGRDGTPGEKGEKGDAGLLGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPRGPKGVSGTPGKHGTPGKKGPKGKKGEPGLPGPCSCGSSRAKSAFSVAVTKSYPRERL 174
                                                                                                                                NQQNHYDGSTGKFYCNIPGLYYFSYHITVY--MKDVKVSLFKKDKAVLFTYDQYQEKNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMYSYEMK-GKSDTSSNHAVLKLAKGDEVWLRM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIKFDKILMNEGGHYNASSGKFVCSVPGIYYFTYDITLANKH-----LAIGLVHNGQ--Y 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPRGER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPGAPGSSGVVGRMGFPGKDGQDGQDGDRGDSGEEGPPGRTGNRGKQGPKGKAGAIGRA 114
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11382781;
                                                                                                                                                                                                                                                                                                                                                21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GQHGPKGEKGYPGIP-----PELQIAFMASLATHFSNQNS
                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                              Score 299; DB 6;
Pred. No. 5.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                  C6253BA803B9A668 CRC64;
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                               Length 240;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                243
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                                                                                                                                                                                                                                                                                                                                30;
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Q95JD7 Q95JD7;

PRELIMINARY;

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RESULT
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Best Local :
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InterPro; IPR000087; Collagen.
InterPro; IPR000087; Collagen.
Pfam; PF001391; Collagen; 1.
ProDom; PD000007; Collagen; 1.
PROSITE; PS01113; C1Q; UNKNOWN_1.
SEQUENCE 243 AA; 26264 MW; 498
                                                                                                                                                                                                                                                                                                                                                                  Q9N178;
01-OCT-2000 (
01-OCT-2000 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                      SEQUENCE FROM N.A.

MEDLINE=21015405; PubMed=11130976;
Nielsen V.H., Bendixen C., Arnbjer
Shukri N.M., Thomsen B.;
    "Abnormal growth plate function in type X collagen.";
Mamm. Genome 11:1087-1092(2000).
EMBL; AF222861; AAF37271.1; -.
InterPro; IPR001073; Clq.
                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    Sus scrota (Pig).
                                                                                                                                                                                                                                                                                                                               COL10A1
                                                                                                                                                                                                                                                                                                                                                  Type X collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9N178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decreased in parallel with reduced insulin sensitiv progression to type 2 diabetes in rhesus monkeys."; Diabetes 50:1126-1133/2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF404407; AAK92202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hotta K., Funahashi T., Bodkin N.L., Hansen B.C., Matsuzawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21232234; PubMed=11334417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae;
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                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Circulating concentrations of the adipocyte protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGP----PGPPGP-----PGIPGNHGNNGATGHEGAKGEKGDKGD----LGPRGERGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH
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75; Conserv
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.5%;
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15,
21,
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                                                                                                                                  Arnbjerg
                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 293.5; DB b;
Pred. No. 1.7e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                        pigs
                                                                                                                                     J.,
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                                                                                        carrying a
                                                                                                                                     Sorensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                     C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                     Jensen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                     H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local
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01-JUN-2002
01-JUN-2002
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BEG1.
Homo sapiens (Human).
Homo sapiens (Human).
Thoria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TE71;
                                                                                                                                                                                                                                                                       Aerbajinai W., Miller J.L.;
Submitted (JAN-2002) to the
EMBL; AY074490; AAL71549.1;
SEQUENCE 1077 AA; 120974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00007; COMPLEMNTC1Q. ProDom; PD000007; Collagen; 2. SMART; SM00110; C1Q; 1.
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pfam; PF00386; C1q; 1.
pfam; PF01391; Collagen; 8.
                        1014
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                                                                                                                                                                                                  34 GLPPDCSKCCHGDYS----FRGYQGPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GYQGPPGPPGPPGIPGNHGNNGNNGATGHEG--AKGEKGDKGDLGP-----RGERGQHG
                                                                                                                                               GATGHEGAKGEKGDKGDLGPRGERGQ--
LFE
                                                                                                                        QVSSPE-RDNETFNSGDSGQGDSRSMTPVDVPVTNPAATILPVHVYP-LPQQMRVAFSAA
                       LMKNEEVLVSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGAIYGSSWKYSTFSGYL
                                     LMHNGNTYFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGFL 241
                                                                                              LATHFS -- NONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGKSDTSSNHAVLKLAKGDEVWLRM---GNGALHGDHQRFSTFAGFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKILYNGQQHYDPKTGIFTCRIPGIYYFSYHI--HVKGTHAWVGLYKNGTPVMYTYDEYV
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                                                                        RTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVN
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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29.6%;
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                                                                                                                                                                                                                                                                         MW;
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                                                                                                                                                                                                                      Score 273; DB 4
Pred. No. 7e-16;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 276.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Ĥomo.
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                                                                                                                                              -HGPKGE----KGYPGIPPELQIAFMAS
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les 87;
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Best Local S
Matches 73
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01-MAR-2001
01-DEC-2001
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Q9H667;
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Q9Z1K4;
                                                    protein).
Homo sapiens (Human).
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InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   failures of chondrocyte patterning and type X collagen expression.";
Int. J. Dev. Biol. 44:309-316(2000).
EMBL; AJ131848; CAA10518.1; -.
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Marks S.A., Lundmark C., Christersson C., Wurtz T., Odgren P.R.
Seifert M.F., MacKay C.A., Mason-Savas A., Popoff S.E.;
"Endochondral bone formation in toothless (osteopetrotic) rats:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
     Mammalia; Eutheria;
                           Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP--TMYTYDEYSKGYLDQASGSAIMELTENDQVWLQLPNAESNGLYSSEYVHSSFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNTVFSMYSYE--MKGKSDTSSNHAVLKLAKGDEVWLRMGN---GALHGDHQRFSTFAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAYPAVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHI~-HVKGTHVWVGLYKN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPGLPGPPGPPGPPSQAVIPDGFTKSGQRPRLSGMPLVSANQGVTGMPVSAFTVILS
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                                                                                                  (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
569 fis, clone HSIO2142 (Hypothetical 17.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                         PRELIMINARY;
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Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10, Created)
10, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 270; DB 11;
Pred. No. 2.8e-16;
                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FF43B1548028813E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                            158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFMASLA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT
Q8TEJ5
В
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                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashii Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka 'Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                              Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; aK074129; BAB84955.1; .
                                                                                                                                                        spleen."
                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01113; C1Q; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 158 AA; 17625 MW; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2001) to the EMBL; AK026222; BAB15398.1; EMBL; BC007520; AAH07520.1;
                                                                                                                                                                                                                                                                                                                                                           Q8TEJ5;
                                                                                                                                                                                                                                                                                                                                                                          Q8TEJ5
                                                                                                       SEQUENCE
                                                                                                                   NON_TER
                                                                                                                                                                                             TISSUE-SPLEEN;
                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                           FLJ00201
                                                                                                                                                                                                                                                                                                       FLJ00201 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00007; COMPLE SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001073; Clq. Pfam; PF00386; Clq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=SMALL INTESTINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                    "The nucleotide sequence of a
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
462 GPSGIPGLQGPAGPIGPQGLPGLKGEPGLPGPPG-EGRAGEPGTAGPTGPPGVPGSPGIT 520
                                                                                                                                                                                  rikuya H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 YPGIPPELQIAFMASLATHFS--NONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHGDHQRFSTFAGFLLFE 244
                        GDYSFRGYQGPPGPPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGE----R
                                                                                                                                                                                                                                                                                                                                                                                                                                        IYGSSWKYSTFSGYLLYQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAPDHETASNHAILQLFQGDQIWLRLHRGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YP-LPQQMRVAFSAARTSNLAPGTLDQPIVEDLLLNNLGETFDLQLGRENCPVNGTYVFI 79
                                                    Similarity 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                    705 AA;
                                                                                                                                                                                  Takano
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                  J.,
                                                                                                    67430 MW; 07DB85A65A948ED3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.5%;
                                                 18.9%; Score 258.5; DB 4; 31.6%; Pred. No. 8.4e-15; Live 24; Mismatches 92;
                                                                                                                                                                                  Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 266.5; DB 4
Pred. No. 2.7e-16;
                                                                                                                                                                   long
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                    Kikuno R., Nagase T., ng cDNA clone isolated
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                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                  update)
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                                                                          Length 705;
                                                  Indels
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RESULT 11
Q96D07
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Q8R002
ID Q8R00
AC Q8R00
DT 01-JU
R Simil
OS Mus m
OC Eukar
OC Mamma
OC Eukar
OC NCBI
RN [1]
RN [1]
RN [2]
RP SEQUE
RA Strau
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RN SEQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR-2002) to the EMBL EMBL; BC023068; AAH23068.1; -.
EMBL; BC025174; AAH25174.1; -.
Hypothetical protein.
SEQUENCE 243 AA; 25420 MW; 4
 Q96D07;
01-DEC-2001
01-DEC-2001
                                               Q96D07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBROO2 PRELIMINARY; PRT; 243 AA.

OBROO2;
Ol-JUN-2002 (TrEMBLrel. 21, Created)
Ol-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to DKE2F58680621 protein (Hypothetical 25.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                      110
                                                                                                                       225
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                                                                                                                    STESGELVY 233
                                                                                                                                                                                                      --LMHNGNTVFSMYSYEMKG---KSDTSSNHAVLKLAKGDEVWLRMGNG---ALHGDHQRF
                                                                                                                                                                                                                                                   ASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVY
                                                                                                                                                                                                                                                                                                                                                                                LLALFFLPFCLCQDEYMESPQTGGLPPDCSK----CCHGDYSFRGYQGPPGPPGPPGIPGN
                                                                                                                                               STFAGFLLF 243
                                                                                                                                                                           FDLVKNGQSIASFFQY-FGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTD
                                                                                                                                                                                                                                  RSESRVPPPADTPLPFDRVLLNEQGHFDPTTGKFTCQVPGVYYFAV----
                                                                                                                                                                                                                                                                                            DGRDGRDGAPGAPGEKGEGGRPGLPGPRGEPGPRGEAGPMGAIGPAGECSVPPRSAFSAK
                                                                                                                                                                                                                                                                                                          HGNNGNNGATGHEGAKGEKGDKGDLGPRGE---RGQHGPKGEKGYPG---IPPELQIAFM 121
                                                                                                                                                                                                                                                                                                                                                   LLALLLLGLV-----SGSPPLDDNKIPSLCPGQ---PGLPGTPGHHGSQGLPGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVLTSPFPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAY----HVHVKGTNVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VALYKNNVPATYTYDEYKKGYLDQASGGAVLQLRPNDQVWVQMPSDQANG-LYSTEYIHS
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                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
 (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                               18.8%; ilarity 32.5%; Conservative 3:
                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
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19,
19,
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Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                             Score 257.5; DB 1
Pred. No. 2.9e-15;
3; Mismatches 100
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498129CD051DB97B CRC64;
 sequence
                                            744
                                            AA
 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length
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                                                                                                                                                                                                                                  HATVYRASLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                            243;
                                                                                                                                                                                                                                                                                                                                                                                                               35;
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                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                  67
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RESULT 12
Q9D2V4
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Best Local
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STRAIN-C57BL/C;; TISSUE-KIDNEY;

MEDLINE-21085660; PubMed-11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Fleischmann W., Gassterland T., Gissi C., King B., Kochiwa H.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci D., Accompanying M., Carninci D., Accompanying M.,

Blake J., Boffelli D., Bojunga N., Carninci D., Accompanying M.,

Rediction M., Tohin M., Barsh G.,

Rediction M., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci D.,
                                                                                                                                                                                                                                                                                                                                                                        Q9D2V4;
Q9D2V4;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013881; AAH13581.1; .
InterPro; IPR001073; C1q.
InterPro; IPR001087; Collagen.
Pfam; PP00386; C1q; 1.
Pfam; PP00386; C1q; 1.
Probom; PP01391; Collagen; 7.
Probom; PD000007; Collagen; 2.
PROSITE; PS01113; C1Q; UNKNOWN_1.
Collagen; Hypothetical protein.
Collagen; Hypothetical protein.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     COL8A1.
                                                                                                                                                                                                                                                                                                                                                      Procollagen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, La Hypothetical 73.4 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAAGLYAGQYVHSSFSGYLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYHV--HCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGKPGALGPQGQPGLPGPPGPPGPPANMPPTPPPQGEYLPDMGLGIDGVKPPHAYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIPGD--QGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGKPGVAGLHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGDKGDLGPRGERGQHGPKGEKGYPGIP------PELQI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
, type VIII, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.8%; Score 257.5; 29.9%; Pred. No. 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                744
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; Murinae; Mus
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Best Local
                                    Submitted (JUL-2001) to the EMBI Submitted (JUL-2001) to the EMBI EMBL; BC011061; AAH11061.1; -. MGD; MGI:88463; CO18a1.

InterPro; IPR001073; C119.

InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
                                                                                                                                                                                                                                                                              0921S8
0921S8;
01-DEC-2001
01-DEC-2001
01-JUN-2002
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Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0007; COMPLEMNTC1Q. SMART; SM00110; C1Q; 1. PROSITE; PS01113; C1Q; 1.
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                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001
 Collagen.
SEQUENCE
                                                                                                                                               Strausberg
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                       COL8A1.
                                                                                                                                                                                                                                                                  Procollagen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
                                                                                                                                                                                          NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                           PROSITE; PS01113; C10; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                    723 AAGLYAGQYVHSSFSGYLLY 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGA------KGE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGDKGDLGPRGERGQHGPKGEKGYPGIP-----PELQI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKPPHAYAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHV--HCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQMPSEQ
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77; Conserv
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IPR000087; Collagen.
 744 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 AA;
                                                                                                                                                                                                                                                                 (TTEMBLrel. 19, Created)
(TTEMBLrel. 19, Last sequence update)
(TTEMBLrel. 21, Last annotation update)
, type VIII, alpha 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                      (Mouse)
                                                                                                                                                                                                         Chordata;
Rodentia;
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   73621 MW;
                                                                                                                                 to the EMBL/GenBank/DDBJ databases
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Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                            PRT;
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   BF7A7FD79D8463AA CRC64;
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                                                                                                                                                                                                                                                                                                                                            744
                                                                                                                                                                                                                                                                                                                                            AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 744;
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RESULT
Q95J95
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Best Local Similarity
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Q95J95;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2001) to the EMELEMBLE AF417206; AAL09702.1; -. InterPro; IPR001073; C1, InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kabir M., Ananthnarayan S., Ionut V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adiponectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dea M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000007; Collagen; 1.
PROSITE; PS01113; C1Q; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Regulation of Adiponectin gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           723 AAGLYAGQYVHSSFSGYLLY 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167
                                                                                                                                                  101 --HGPKGEKGYPGIPPEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                     54 GP----PGPPGP-----PGIPGNHGNNGNNGATGHEGAKGEKGDKGD---LGPRGERGQ- 100
                                                                                                                                                                                                  1 GPGVLLPLPKGACPGWMAGIPGHPGHNGTPGRDGRDGTPGEKGEKGDPGLVGPKGDTGET 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHV--HCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQASGSAVLLLRPGDQVFLQMPSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTCEVPGVYYFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGVKPPHAYAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGDKGDLGPRGERGQHGPKGEKGYPGIP-----PELQI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIPGD--QGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGKPGVAGLHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLPPDCSKCCHGDYSFRGYQGPPGPPGPPGIPGNHGNNGNNGATGHEGA------
                                                                                                  GVTGVEGPRGFPGTPGRKGEPGESAYVHRSAFSVGLESRITVPNVPIRFTKIFYNLQNHY
DGTTGKFHCNIPGLYYFSYHITVY--LKDVKVSLYKKDKAMLFTYDQYQEKNVDQASGSV 178
                                                DVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -GALHGDHQRFSTFAGFLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00386; C1q; 1.
PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bergman R.N.;
                                                                                                                                                                                                                                                                                                                                                                                                             194
194 AA;
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1 (TrEMBLrel. 19,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -AFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%;
29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                             20890 MW; 3AA3D947D187AF9A CRC64;
                                                                                                                                                                                                                                                                                                     18.1%; Score 247.5;
30.9%; Pred. No. 1.7e
tive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 257; DB 11;
Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                  --- QIAFMASLATHFSNQNSGIIFSSVETNIGNFF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                             1.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                          DB 6;
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                                                                                                                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the fat-fed dog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Citters G.W.,
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                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                        Length 194;
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                                                                                                                                                                                                                                                                                                          27;
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VLKLAKGDEVWLRM

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Query Match
Best Local Similarity
Watches 71; Conserva
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Q9DCM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI-88223; Ciqa.
InterPro; IPR001073; Ciq.
InterPro; IPR001087; Collagen.
Pfam; PP00386; Ciq; 1.
Pfam; PP01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTCIQ.
SMART; SM00110; CiQ; 1.
PROSITE; PS01113; CiQ; 1.
PROSITE; PS01113; CiQ; 1.
SEQUENCE 245 AA; 25974 MW; 41C2066D49592020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F., Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK002655; BAB22262.1; -.
EMBL; BC002086; AA-02086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9DCM6:
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Complement component 1, q subcomponent, alpha polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Matsuo Y., Nikaido I., Pesole G., Quackenbush C., Schriml I., Pesole G., Quackenbush C., Schrimland R., Schrimland
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                   154 RFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG--NTVFSMYSYEMKGKSDTSSNHAVLK 211
150 RFICAVPGEYYFNFQVISKWDL-CLFIKSSSGGQPRDSLSFSNTNNKGLFQVLAGGTVLQ 208
                                                                                                                             91
                                                                                                                                                                                          95
                                                                                                                                                                                                                                       51 GYOGPPGPPGPPGIPGNHGNNGNNGATG-HEGAKGEKGDKGD------LGP 94
                                                                                                                   LGDSGPQGLKGVKGNPGNIRDQPRPAFSAIRQNPMTLGNV-VIFDKVLTNQESPYQNHTG 149
                                                                                                                                                          RGERGQHGPKGEKGYPG-IPPELQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTG 153
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                 17.5%; Score 239.5; DB 11; Length 245; 33.2%; Pred. No. 1.2e-13; tive 26; Mismatches 94; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                    23;
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Search completed: January 15, 2003, 19:39:47 Job time : 94 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
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1367
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11:
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14:
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1367	100.0	246	9	US-10-036-041-2	Sequence 2, Appli
2	1367	100.0	246	9	US-10-035-855-2	Sequence 2, Appli
ω	1367	100.0	246	12	US-10-036-342-2	:-
4	294	21.5	247	10	US-09-776-976-4	
Մ	294	21.5	247	10	US-09-758-055-4	Sequence 4, Appli
6	294	21.5	247	10	US-09-909-547-4	4,
7	293.5	21.5	244	9	US-09-911-176B-48	8,
8	293.5	21.5	244	10	US-09-776-976-6	•
9	293.5	21.5	244	10	US-09-758-055-6	9
10	293.5	21.5	244	10	US-09-909-547-6	Sequence 6, Appli
11	293	21.4	247	10	US-09-776-976-2	Sequence 2, Appli
12	293	21.4	247	10	US-09-758-055-2	Sequence 2, Appli
13	293	21.4	247	10	US-09-909-547-2	Sequence 2, Appli
14	290.5	21.3	259	9	US-09-992-598-47	Sequence 47, Appl
15	290.5	21.3	259	9	US-09-989-293A-47	Sequence 47, Appl
16	290.5	21.3	259	9	US-09-989-735-47	Sequence 47, Appl
17	290.5	21.3	259	9	US-09-990-444-47	Sequence 47, Appl
18	290.5	21.3	259	9	US-09-989-730-47	47,
19	290.5	21.3	259	9	US-09-990-436-47	Sequence 47, Appl

45	44	43	42	41	40	39	38	37	36	35	34	ω S	32	<u>3</u> 1	30	29	28	27	26	25	24	23	22	21	20
264.5	264.5	264.5	273	273	287	289.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5	290.5
19.3	19.3	19.3	20.0	20.0	21.0	21.2	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3
243	243	243	746	746	247	278	259	259	259	259	259	259	259	259	259	259	259	259	259	259	259	259	259	259	259
9	9	9	10	9	9	10	12	10	10	10	10	10	10	10	10	10	10	10	10	9	ø	9	9	9	9
US-09-944-896-42	US-09-944-403-42	US-09-944-413-42	US-09-738-973-185	US-09-854-133-185	US-09-911-176B-3	US-09-799-777-35	US-10-052-586-62	US-09-989-721-47	US-09-990-456-47	US-09-993-604-47	US-09-991-163-47	US-09-990-442-47	US-09-991-073-47	US-09-989-732-47	US-09-989-731-47	US-09-989-727-47	US-09-989-279-47	US-09-989-723-47	US-09-989-722-47	US-10-176-758-62	US-10-174-590-62	US-09-997-653-47	US-09-989-734-47	US-09-993-687-47	US-09-991-181-47
	Sequence 42, Appl	Sequence 42, Appl	Sequence 185, App	Sequence 185, App	Sequence 3, Appli	Sequence 35, Appl	Sequence 62, Appl		47		Sequence 47, Appl		Sequence 47, Appl		47		Sequence 47, Appl	Sequence 47, Appl	_		Seguence 62, Appl			Sequence 47, Appl	Sequence 47, Appl

ALIGNMENTS

RESULT 1 US-10-036-041-2

Sequence 2, Application US/10036041 Publication No. US20020192751A1 GENERAL INFORMATION: APPLICANT:
APPLICANT: PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/085579 CURRENT APPLICATION NUMBER: US/10/036,041
CURRENT FILING DATE: 2001-12-26 TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3030R1C8 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan L. PRIOR PRIOR APPLICANT: OR APPLICATION NUMBER: 60/11552
OR FILING DATE: 1999-01-12
OR APPLICATION NUMBER: 60/116843
OR FILING DATE: 1999-01-22
OR APPLICATION NUMBER: 60/125774
OR FILING DATE: 1999-03-23
OR APPLICATION NUMBER: 60/125778 FILING DATE: 1998-12-23
APPLICATION NUMBER: 60/114140
FILING DATE: 1998-12-23 APPLICATION NUMBER: 60/113605 FILING DATE: 1998-12-23 APPLICATION NUMBER: 60/113621 FILING DATE: 1998-12-22 APPLICATION NUMBER: 60/113430 FILING DATE: 1998-12-23 Goddard, Audrey Godowski, Paul J Watanabe, Colin K. Wood, William I. Pan, James Gurney, Austin L. Stewart, Timothy A.

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FILING DATE: 2000-03-02
APPLICATION NUMBER: PCT/US00/14042
FILING DATE: 2000-05-22
APPLICATION NUMBER: PCT/US00/15264
                               FILING DATE: 2000-08-23
APPLICATION NUMBER: PCT
FILING DATE: 2000-08-24
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                                                                                     FILING DATE: 2000-06-02
APPLICATION NUMBER: PCT/US00/23522
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APPLICATION NUMBER: FILING DATE: 2000-1
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RESULT 2
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SEQ ID NO 2
LENGTH: 246
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10035855 Publication No. US20030008348A1
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                                          PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-12-22
                                                                                                   PRIOR APPLICATION NUMBER: 60/085579 PRIOR FILING DATE: 1998-05-15
                                                                                                                              CURRENT APPLICATION NUMBER: US/10/035,855
                                                                                                                                                           TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3030R1C4
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TYPE: PRT
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PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
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| 241 LLFETK 246
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APPLICATION NUMBER: PCT/US99/30720
FILING DATE: 1999-12-22
APPLICATION NUMBER: PCT/US00/05601
                                                                                                         FILING DATE: 1999-05-14
APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02
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FILING DATE: 2001-07-18
APPLICATION NUMBER: PCT/US99/10733
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APPLICATION NUMBER: 09/869599
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APPLICATION NUMBER: 09/874503
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FILING DATE: 1999-05-14
APPLICATION NUMBER: 09/380142
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FILING DATE: 1999-06-08
APPLICATION NUMBER: 60/144791
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FILING DATE: 1999-04-27
APPLICATION NUMBER: 60/132371
FILING DATE: 1999-05-04
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FILING DATE: 1999-05-04
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FILING DATE: 1999-04-27
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FILING DATE: 1999-04-21
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FILING DATE: 1999-04-13
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FILING DATE: 1999-03-23
APPLICATION NUMBER: 60/125778
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                                                                                                                                            APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Godowski, Nastin
                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                            APPLICANT:
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APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3030R1C5
                                                                                                APPLICANT:
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FILING DATE: 2000-12-20
APPLICATION NUMBER: PCT/US01/06520
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FILING DATE: 2000-08-24
APPLICATION NUMBER: PCT/US00/32678
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FILING DATE: 2000-06-02
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                                                                            Watanabe, Colin | Wood, William I.
                                                                                                                                              Gurney, Austin L.
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Godowski, Paul J.
                                                                                                            Stewart, Timothy A
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PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
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JRRENT FILING DATE: 2001-12-26
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DR FILING DATE: 1999-04-27
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DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/131291
DR FILING DATE: 1999-04-27
DR APPLICATION NUMBER: 60/132371
DR FILING DATE: 1999-05-04
DR APPLICATION NUMBER: 60/132379
DR APPLICATION NUMBER: 60/132379
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OR APPLICATION NUMBER: 60/113605
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/113621
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/114140
OR FILING DATE: 1998-12-23
OR APPLICATION NUMBER: 60/115552
OR FILING DATE: 1999-01-12
OR FILING DATE: 1999-01-12
                                                               DR APPLICATION NUMBER: 09/747259
DR FILING DATE: 2000-12-20
PR APPLICATION NUMBER: 09/816744
DR FILING DATE: 2001-03-22
DR APPLICATION NUMBER: 09/854208
DR FILING DATE: 2001-05-10
DR APPLICATION NUMBER: 09/854280
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FILING DATE: 1999-10-29
APPLICATION NUMBER: 09/311832
FILING DATE: 1999-05-14
APPLICATION NUMBER: 09/380142
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FILING DATE: 1999-06-08
APPLICATION NUMBER: 60/144791
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APPLICATION NUMBER: 60/135750
FILING DATE: 1999-05-25
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APPLICATION NUMBER: 60/127706
FILING DATE: 1999-04-05
APPLICATION NUMBER: 60/129122
FILING DATE: 1999-04-13
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APPLICATION NUMBER: 60/132383
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FILING DATE: 1999-04-21
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APPLICATION NUMBER: 60/125826
FILING DATE: 1999-03-24
APPLICATION NUMBER: 60/127035
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FILING DATE: 1999-03-23
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FILING DATE: 1999-01-22
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FILING DATE:
APPLICATION NUMBER: 09/874503
FILING DATE: 2001-06-05
APPLICATION NUMBER: 09/869599
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Best Local Similarity
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PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
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APPLICATION NUMBER: PCT/US01/19692
FILING DATE: 2001-06-20
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FILING DATE: 2000-03-02
APPLICATION NUMBER: PCT/US00/14042
FILING DATE: 2000-05-22
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APPLICATION NUMBER: PCT/US01/06520
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APPLICATION NUMBER: PCT/US00/15264
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FILING DATE: 1999-05-14
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APPLICATION NUMBER: PCT/US00/34956
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LLFETK 246
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                                                                                YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF 240
                                                                                                                                                                                       PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF
                                                                                                                                                                                                         PPGIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPELQIAF 120
                                                                YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRFSTFAGF
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2001-06-29
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Pred. No. 9.9e-112;
; Mismatches 0;
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RESULT 4
US-09-776-976-4
; Sequence 4, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim

120 180

180

60 60

0;

APPLICANT:

Erickson, Mary Ruth

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PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 4
LENGTH: 247
TYPE: PRT
ORGANISM: mus musculus
US-09-776-976-4
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SEQ ID NO 4
TWICTH: 247
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Best Local
                                                                                                                                 APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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APPLICANT: Erickson, Mary I
APPLICANT: Yen, Frances
                                                                                       NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patent.pm
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PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
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CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
ORGANISM: mus
                        TYPE: PRT
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musculus
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Best Local Similarity
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PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 7
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PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US6.CIP
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109 EAAYMYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHIT 168
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                                                                                                                        64 IPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGER----GQHGPKGEKGYPGIPPE-----
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                                       -----LQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMM 170
                                                                                HPGHNGTPGRDGTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPGTPGRKGEPG 108
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Yen, Frances
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31.5%; Pred. No. 1.5e-18;
tive 40; Mismatches 102;
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US-09-776-976-6
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ANTIBODIES THAT BIND AN
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROT
FILE REFERENCE: 97-30D1
CURRENT APPLICATION UNMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
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                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09776976 Patent No. US20020037849A1
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LENGTH: 244
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Patent No. US20020156247371
  PRIOR APPLICATION NUMBER: US 09/758,055 PRIOR FILING DATE: 2001-01-10 PRIOR APPLICATION NUMBER: US 60/176,228 PRIOR FILING DATE: 2000-01-14 PRIOR APPLICATION NUMBER: US 60/198,087 PRIOR FILING DATE: 2000-04-13
                                                                                                                 CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
                                                                                                                                                   APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                                  APPLICANT: Fruebis, Joachim APPLICANT: Erickson, Mary
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SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Homo sapiens
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34.5%;
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Pred. No. 1.7e-18;
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SEQ ID NO 6
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TYPE: PRT
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; ORGANISM: Homo sapiens US-09-758-055-6
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Best Local Similarity
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APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: 0B63 Globular Head and Uses Thereof for Decreasing Body Mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-01-10 PRIOR APPLICATION NUMBER: US 60/176,228 PRIOR FILING DATE: 2000-01-14
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CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                         148 FDVMTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNH 207
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nes 76; Conserv
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YDGSTGKFHCNIPGLYYFAYHITVY--MKDVKVSLFKKDKAMLFTYDQYQENNVDQASGS
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34.5%; Pred. No. 1.7e-18;
htive 35; Mismatches 78;
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Pred. No. 1.7e-18;
35; Mismatches 78
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; ORGANISM: Homo
US-09-909-547-6
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CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                   Sequence 2, Application US/09776976 Patent No. US20020037849A1 GINERAL INFORMATION:
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FILE REFERENCE: 76.US4.REG
CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
                                                                       APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                          APPLICANT: Fruebis, Joachim APPLICANT: Erickson, Mary F
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SOFTWARE: Patent.pm
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TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
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76; Conserv
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Pred. No. 1.7e-18;
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SEQ ID NO 2
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Best Local Similarity
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APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.US4.REG
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/758,055
CURRENT FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
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SOFTWARE: Patent.pm
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TYPE: PRT
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TYPE: PRT
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LLLQALLFLLILP-SHAEDDVTTTEELAPALVPPPKGTCA---
                                 LIYWQLLALFFLPFCLCQDEYMESPQTGG--LPPDCSKCCHGDYSFRGYQGPPGPPGPPG 63
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Pred. No. 1.9e-18;
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Mismatches
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US-09-909-547-2
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PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR APPLICATION NUMBER: US 60/299,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
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LENGTH: 247
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Patent No. US20020091080A1
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CURRENT FILING DATE: 2001-07-19
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TITLE OF INVENTION: OBG3 Globular Head and
FILE REFERENCE: 76.US6.CIP
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224 HNGLYADNVNDSTFTGFLLF 243
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Local Similarity 31.2%;
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                                                                   HITVY--MKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGD
                                 --ALHGDHQRESTFAGFLLF 243
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US-09-992-598-47; Sequence 47; Application US/09992598
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CURRENT APPLICATION NUMBER: US/09/92,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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RR APPLICATION NUMBER: 60/01 RF FILING DATE: 1998-06-04 RR APPLICATION NUMBER: 60/01 RR APPLICATION NUMBER: 60/01 RF FILING DATE: 1998-06-04 RR FILING DATE: 1998-06-04 RR PILING DATE: 1998-06-04 PR PILING DATE:
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                FILING DATE: 1998-06-04
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Baker, Kevin P.
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Stewart, Timothy A.
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Godowski, Paul J.
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DR FILING DATE: 1998-06-25
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DR APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/090862
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-KGEMGSPGAP--CQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAA
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78; Conser
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34; Mismatches
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FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-19

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APPLICATION NUMBER:

60/090246

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APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17

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60/089532 60/089514 60/089512 60/089440

FILING DATE: 1998-06-16 APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-06-16

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-16

FILING DATE:

APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-11 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876

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FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-06
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60/088861 60/088858 60/088826 60/088824 018880/09

APPLICATION NUMBER: APPLICATION NUMBER: 60/0FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: FILING DATE:

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60/088202 60/088167 60/088326 60/088033

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APPLICATION NUMBER: 60/088217

FILING DATE: 1998-00 APPLICATION NUMBER:

60/089803

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FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-22

APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C66

CURRENT APPLICATION NUMBER: U5/09/989,293A

CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065316
PRIOR APPLICATION NUMBER: 60/065311
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Botstein, David
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Ferrara, Napoleone
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<u>ب</u> 235pp; English.

cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences Anz61606-261832 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences Anz61606-261649, Anz61725-261765, Anz61802-261811 and Anz61826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences Anz61650-261668, Anz61766-261780, Anz61812-261817 and Anz61827-261829 encode proteins with one or more putative dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhabit the growth of transmembrane domains. relates to novel nucleic acid sequences derived from

Sequence 1123 B₽; 277 A; 266 Ç 321 G; 258 Η, other;

밁 Qγ В δÃ Percent Similarity:
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Query Match: δÃ δõ В δõ 밁 QY 밁 Ş В B δÃ 밁 Ş Q Q 밁 Ď, US-10-036-041-2 (1-246) Alignment Мо :: 201 720 181 660 161 600 141 540 121 480 101 420 360 300 240 180 41 81 61 21 μ GluThrAsnIleGlyAsnPhePheAspValMetThrGlyArgPheGlyAlaProValSer 160 ProProGlyIleProGlyAsnHisGlyAsnAsnGlyAsnAsnGlyAlaThrGlyHisGlu AGTGTTGCCATGGAGATTATGGATTCCGTGGTTACCAAGGGCCCCCTGGACCCCCAGGT LysCysCysHisGlyAspTyrSerPheArgGlyTyrGlnGlyProProGlyProProGly SerAspThrSerSerAsnHisAlaValLeuLysLeuAlaLysGlyAspGluValTrpLeu GGCGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGACGTGGAAGTGTATGTG GlyValTyrPhePheThrPheSerMetMetLysHisGluAspValGluGluValTyrVal 180 MetAlaSerLeuAlaThrHisPheSerAsnGlnAsnSerGlyIleIlePheSerSerVal 140 HisGlyProLysGlyGluLysGlyTyrProGlyIleProProGluLeuGlnIleAlaPhe GGGGCCAAGGGTGAGAAAGGAGACAAAGGCGGACCTGGGGGCCTCGAGGGGAACGGGGGCAG CCTCCTGGCATTCCAGGAAACCATGGAAACAATGGAAATAACGGAGCCACTGGCCACGAA CTGTGTCAAGATGAATACATGGAGTCTCCACAAGCTGGAGGACTGCCCCAGACTGCAGC LeuCysGlnAspGluTyrMetGluSerProGlnThrGlyGlyLeuProProAspCysSer 40 TyrLeuMetHisAsnGlyAsnThrValPheSerMetTyrSerTyrGluMetLysGlyLys GAGACCAACATTGGAAACTTCTTCGATGTCATGACTGGTAGATTTGGGGGCCCCCGTATCA ATGGCTTCTCTAGCGACTCACTTCAGCAATCAGAACAGTGGCATTATCTTCAGCAGTGTT CATGGCCCCAAAGGATAGAAGGGATACCCAGGGGTGCCACCAGAGCTGCAGATTGCGTTC 3.36e-95 1311.00 97.15% 95.93% 95.93% 21 x AAZ61633 (1-1123)Gaps: Mismatches: Matches: Conservative: Indels: 1123 236 3 7 0 419 539 479 9, 60 719 599 359 299

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                                                                                   The invention relates to novel nucleic acid sequences derived from rat . CC dermal papilla, human keratinocytes and meonatal foreskin fibroblasts, CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying ccells. Polypeptides of the invention may be used to treat inflammation, CC cancer and neurological diseases: The proteins may be used to stimulate ct the growth and motility of keratinocytes, to inhibit the growth of CC cancer cells, to modulate anajogenesis and tumour vascularisation, to conclude to treat inflammation, to modulate epithelial cell growth and to CC inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle CC disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived CC from several mouse, rat or human skin cell types. Sequences CC AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode CC proteins with an N-terminal signal sequence, indicating that the proteins CC are secreted. Sequences AAZ6160-Z61668, AAZ61766-Z61780, AAZ61812-Z61817 CC and AAZ61827-61829 encode proteins with one or more putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 137; 235pp; English
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09-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1999
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developmental disorder; skin wound; hair follicle disorder;
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
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Sequence 203, Application US/0918893

Batent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Is
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FILE REFERENCE: 11000.1011c1
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SEQ ID NO 203
LENGTH: 1123
TYPE: DNA
ORGANISM: Rat
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CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
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Percent Similarity:
APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Steaman, Matthew APPLICANT: Onrust, Rene APPLICANT: Murison, James Gre APPLICANT: Murison, James Gre INVENTION: Compositi
                                                               GENERAL INFORMATION:
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